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Wild-type human

Human protein

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Protein C Protein C Protein C

Minimum DB Maximum DB

Database

Result Š

Searched:

Sequence:

Protein Protein

Protein Protein

Protein Protein

Protein Protein Protein

Protein Protein

seqidl_mod.rag

OM protein

Run on:

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/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                  AAY18303
AAB36402
                                                                                                                                                                                                                                                                                                                                                                                         AAU99013
AAU99014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99019
                                                      AAY18309
                                                                                                          AAY56803
                                                                                                                                                                                             aab36896
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                                        AAX18297
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                                                                                                                                                                                                                       AAB3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US22152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-1998;
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Synthetic.
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Human protein C de
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Modified GLA domai
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167.515 Million cell updates/sec
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| SIDSZ/gcgdata/geneseqp-embl/AA1980.DAT:*
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| SIDSZ/gcgdata/geneseqp/embl/AA1991.DAT:*
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| SIDSZ/gcgdata/geneseqp/embl/AA1997.DAT:*
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                                                                                           May 15, 2003, 13:23:56 ; Search time 35 Seconds
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           5.1.4_p5_4578
Compugen Ltd.
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                                                                                                                                                                                                                                              908470 seqs, 133250620 residues
             version 5 - 2003 (
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                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAE08629
AAB82675
AAB82676
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AAE08630
                                                                  protein search, using sw model
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AAE08627
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Gapop 10.0 , Gapext 0.5
           GenCore
Copyright (c) 1993
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seq length: 200000000
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Match Length
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Perfect score:
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179
179
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Gaps

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Sequence

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disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative.
protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "cleavage makes a 2-chain inactive
precursor (155-amino acid light chain
attached via a disulfide bond to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein C; human; coronary syndrome; thrombosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein C derivative (H100/S11G/Q32E/N33D/L194S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Gln in wild-type protein"
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                                                                                                                                                                                                                                                                                                                                                                                                    90.9%; Score 179; DB 22; 79.5%; Pred. No. 1.4e-21; 1ve 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Ser in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB82677 standard; Protein; 419 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001 (first entry)
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Best Local Similarity 79.5'
Watches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     419 AA;
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Disulfide-bond
Disulfide-bond
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                domain. The invention relates to a vitamin R-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepais; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion;
                                                                                                                                                          This sequence represents a modified GLA (gamma-carboxyglutamic acid)
                                          Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thromboembolism; prothrombotic disorder; gene therapy; thalassaemia
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                                                                                                                                                                                                                                                                                                                                                                                                           90.9%; Score 179; DB 20; 100.0%; Pred. No. 1.3e-22;
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                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein C derivative #4.
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                                                                                                           Claim 9; Page 79; 86pp;
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WPI; 1999-288309/24.
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Gaps

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Claim 5; Page 54-55; 63pp; English.
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14-MAR-2000; 2000US-0189197.
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                                                                                                                                                                          (ELIL ) LILLY & CO ELI
                                                                                                                                                                                  Gerlitz BE, Jones BE;
                                                                                                                                                                                           WPI; 2001-496919/54.
                                                                                                                                                                                               N-PSDB; AAH26365.
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                                                                        Peptide
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patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed). cleavage makes a 2-chain inactive precursor (155amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)" Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S). myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy; Length 419; Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occinatos disorder. Indels 44 1 ANSFLEELRQGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44 1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 6 in wild-type protein" note- "Gln in wild-type protein" note= "Asn in wild-type protein" 'note= "Thr in wild-type protein" 'note= "His in wild-type protein" Score 179; DB 22; Pred. No. 1.4e-21; 0; Mismatches 9; "gamma-carboxylated" "gamma-carboxylated" 'note= "gamma-carboxylated" /note- "gamma-carboxylated" 'note= "gamma-carboxylated' note- "Leu in wild-type Location/Qualiflers note= "Gla domain" 0..69 AAB82678 standard; Protein; 419 AA Query Match 90.9%; Best Local Similarity 79.5%; Matches 35; Conservative note- "Ser (first entry) notenote-/note-64 419 AA; Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference mutant; mutein. Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Modified-site Modified-site Modified-site Cleavage-site Modified-site Homo sapiens. 15-0CT-2001 Synthetic AAB82678; Seguence Domain RESULT 4 AAB82678 g ប្បវន្តន ð The present sequence is that of a claimed human protein c derivative in which His at position 10 of the mature wild-type protein c sequence (see AMB2673) is substituted with Gln, Ser at position 11 with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. It is an example of protein C derivatives of the invention that have at least 2 annion acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoaquiable states, sepsis (in combination with bactericidal permeability increasing protein of with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human 188..169 /note= "activation peptide; removal activates the 2-chain zymogen" Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -262-amino acid heavy chain)" note= "thrombin cleavage site" "gamma-carboxylated" note- "gamma-carboxylated" note= "gamma-carboxylated" note= "gamma-carboxylated" note= "gamma-carboxylated" note- "gamma-carboxylated" note- "gamma-carboxylated" note- "gamma-carboxylated" note- "N-glycosylated" 'note- "N-glycosylated" note- "N-glycosylated" 'note- "N-glycosylated"

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Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                          Modified GLA domain of vitamin K-dependent protein.
                                                                                  AAY18301 standard; peptide; 44 AA.
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nelsestuen GL;
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Synthetic.
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                                                                                                                           AAY18301;
                                                                                                                                                                                                                                                                         therapy.
                                           RESULT 5
AAY18301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial
                                                                                                                                            /note= "activation peptide; removal activates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular grafts. Human
prothrombotic disorders may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -
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Pred. No. 1.4e-21;
0; Mismatches 9;
                                                                                                                                                                                                        note- "thrombin cleavage site"
                                                            'note= "gamma-carboxylated"
                     note= "gamma-carboxylated'
                                                                                                   'note= "gamma-carboxylated'
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                                                                                                                                                                    2-chain zymogen'
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Best Local Similarity 79.5%;
Matches 35; Conservative
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14-MAR-2000; 2000US-0189197
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Modified-site
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patients with
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                                                                                                                        Peptide
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1..44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic
acid"

98WO-US22152. 97US-0955636.

Location/Qualifiers

domain; mutein; vitamin K-dependent protein; clotting disorder;

(first entry)

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                               This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared its the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                              Length 44;
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Pred. No. 4.1e-22;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE08627 standard; Protein; 419 AA.
Claim 9; Page 82; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein C derivative #1.
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Local Similarity 97.7%;
hes 43; Conservative
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                                                                                                                                                                                                                                  44 AA;
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Matches
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Gaps

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Indels 44

1 ANSFLEELRQGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH

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The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombia activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angins; and disease states predisposing to thrombosis; vascular ocalusive disorders and hypercoagulable states e.g. thrombosis; vascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral heemorrhagic fever and heemolytic uremic syndrome; sepsis in combination with bacterial hemmolytic uremic syndrome; sepsis in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral corpusating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thrombocmbolism; prothrombotic disorder; gene therapy; thalassaemia.
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                                                                                                                                                                                                                                                                           02-FEB-2001; 2001WO-US01221.
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N-PSDB; AAD15225.
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                                                                                                                                                  Homo sapiens.
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AAE08629;
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 Length 419;
88.3%; Score 174; DB 22; Length 4 77.3%; Pred. No. 1e-20; ive 0; Mismatches 10; Indels
                                                                                               1 ANSFLEELRHGSLERECIEEICOFEEAKEIFEDVDDTLAFWSKH 44
                                                                          1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                         AAE08628 standard; Protein; 419 AA.
                                                                                                                                                                                                                                                                                   01-NOV-2001 (first entry)
 Query Match 88.3
Best Local Similarity 77.3
Matches 34; Conservative
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Human; protein C derivative; anticoagulation activity; thrombosis;

Human; protein C derivative; anticoagulation activity; thrombosis;

Human protein C derivative #2.

AAE08628;

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The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type brotein C. Protein C derivatives are useful. In the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angins; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. thrombosis; vascular coagulation (DIC), burns, transplantations, thalassasemia, sickle cell disease, viral heamorrhagic fever and hamolytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thrombotism or stemosis in coronary, cerebral
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serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral heamorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
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Best Local Similarity 77.3%; Pred. No. 1e-20;
Matches 34; Conservative 0; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-2001; 2001WO-US01221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-2000; 2000US-0181948.
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                                                                                                                                                                                                                                               Homo sapiens.
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Human protein C derivative (S11G/Q32E/N33D/L194S).
                                             Protein
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                                                                                                                                               Ношо
   The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular coclusive disorders and hypercoagulable states e.g. thrombosis; vascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial with an anti-platelet agent; protein C describency; acute arterial chrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders
            vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion.
                                                                                                                                                                                                                                                                                                                                                                                                                    Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
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serpin inactivation; acute coronary syndrome; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by gene therapy. The present sequence is human protein C derivative.
                                                                     thromboembolism; prothrombotic disorder; gene therapy; thalassaemia
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Pred. No. 1e-20;
0; Mismatches 10;
                                                                                                                                                         /note= "Encoded by CAA"
                                                                                                                                                                                                                                                                                                                                                  Jones BE;
                                                                                                                    Location/Qualifiers
10
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                                                                                                                                                                                                                                                02-FEB-2001; 2001WO-US01221
                                                                                                                                                                                                                                                                                                                                                  Grinnell BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                     (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-514662/56.
N-PSDB; AAD15227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 AA;
                                                                                                                                            Misc-difference
                                                                                                                                                                                      WO200159084-A1
                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 34;
                                                                                                                                                                                                                   16-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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AAB82675 standard; Protein; 419

RESULT 9 AAB82675 (first entry)

15-OCT-2001

AAB82675;

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/note= "activation peptide; removal activates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "cleavage makes a 2-chain inactive
precursor (155-amino acid light chain
attached via a disulfide bond to a
             myocardial infarction, vascular occlusive disorder, hypercoagulation, sepsis, protein C deficiency, occlusion, thromboembolism; stenosis; antibacterial; immunosuppressive, thrombolytic; cardiant; antianginal; anticoagulant; therapy,
   angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           attached via a disulfide bon
262-amino acid heavy chain)"
                                                                                                                                                                                         'note= "Ser in wild-type protein"
                                                                                                                                                                                                                                                                                    "note= "Leu in wild-type protein"
   coronary syndrome; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note- "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "gamma-carboxylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "gamma-carboxylated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "gamma-carboxylated'
                                                                                                                                                                                                                          "Gln in wild-type
                                                                                                                                                                                                                                                    note= "Asn in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2-chain zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-glycosylated"
                                                                                                                                                           Location/Qualiflers
                                                                                                                                                                                                                                                                                                                   note≐ "Gla domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JAN-2001; 2001WO-US00020.
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                                                                                                                                                                                                                                                                                                                                    69..
                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note-
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C; human;
                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                        Misc-difference
                                                                             mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
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                                                                                                                          Synthetic.
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/note- "activation peptide; removal activates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute
                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                            "cleavage makes a 2-chain inactive
/note= "Ser in wild-type protein"
                                        "Gln in wild-type protein"
                                                                                                                                                          note= "Thr in wild-type protein"
                                                                                                                    note- "Leu in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note- "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note- "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note- "gamma-carboxylated"
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                                                                            note- "Asn in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -chain zymogen'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-glycosylated"
329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "N-glycosylated"
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                                                                                                                                                                                                'note= "Gla domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-2001; 2001WO-US00020
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14-MAR-2000; 2000US-0189197
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                                                                                                                                                                                                                                          59..64
30..89
                                        'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-496919/54.
                                                         Misc-difference 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH26364
                   Misc-difference
                                                                                                 Misc-difference
                                                                                                                                       Misc-difference
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Disulfide-bond
Disulfide-bond
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Disulfide-bond
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                                                                                                                                                                                                                     Disulfide-b
Disulfide-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                               Domain
  ö
                                                                                                                                                                                                                                                                                                                               The present sequence is that of a claimed human protein C derivative in which Ser at amino acid position 11 of the mature wild type protein C sequence (see AAB82673) is substituted with C Gly, Gln at position 32 with Glu, Ann at position 33 with Asp, and Leu at position 194 with Ser. The protein is an example of protein c derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild type protein. A method of producing the derivatives as using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina).

**Combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial combination with genetically protein or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                 Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein C; human; coronary syndrome; thrombosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein C derivative (S11G/Q32E/N33D/t194S/T254S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 174; DB 22;
Pred. No. 1e-20;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key Location/Qualifiers Misc-difference 11
                                                                                                                                                                                                                                                                                               Claim 3; Page 52-53; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB82676 standard; Protein; 419 AA.
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              02-FEB-2000; 2000US-0179801
14-MAR-2000; 2000US-0189197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
                                                                            (ELIL ) LILLY & CO ELI
                                                                                                               Gerlitz BE, Jones BE;
                                                                                                                                                      WPI; 2001-496919/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                             N-PSDB; AAH26363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutant; mutein.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY18299;
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                                                                                                                  The present sequence is that of a claimed human protein C derivative
in which Ser at position 11 of the mature wild-type protein C
sequence (see AAB2670) is substituted with Gly, Gln at position 32
with Glu, Asn at position 33 with Asp. Leu at position 194 with Ser,
and Thr at position 254 with Ser. It is an example of protein C
derivatives of the invention that have at least 2 amino acid
substitutions, but which have increased anticoagulant activity and
resistance to inactivation by serpins compared with the wild-type
protein. A method of producing the derivatives are useful for
protein, while retaining the biological activity of the wild-type
protein, a method of producing the derivatives are useful for
treating coronary syndromes and disease states predisposing to
thrombosis (e.g. mycoardial infarction and unstable anglana).

Combination with bactericidal permeability increasing protein or
with tissue factor pathway inhibitor), thrombocic disorders (in
combination with an anti-platelet agent or by local delivery through
an intracoronary catheter), protein C deficiency, acute arterial
combination with genetically protein C deficiency, acute arterial
thrombocic occlusion, thromboembolism, or stenosis in coronary,
cerebral or peripheral arteries or in vascular grafts. Human
patients with genetically predisposed prothrombotic disorders may
be treated by gene therapy (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Misc-difference 1..44

/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 174; DB 22; Length 4
Pred. No. 1e-20;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
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arterial thrombotic occlusion, and thromboembolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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                                                                    Page 53-54; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY18298 standard; peptide; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MINU ) UNIV MINNESOTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9920767-A1
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                                                                Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY18298;
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\begin{array}{c} \mathbf{F} \times \mathbf{G} \times \mathbf{G} \\ \mathbf{
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                                                                                                                                                   This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
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Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANSFLXXLRQSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 173; DB 20;
Pred. No. 1.3e-21;
0; Mismatches 1;
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                                                                                             Claim 7; Page 78; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.8%;
97.7%;
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Best Local Similarity
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Misc-difference 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 AA;
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/note- "Xaa- gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                         GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                domain of vitamin K-dependent protein.
                                                                                                                                                                                                        Location/Qualifiers
                AAY18297 standard; peptide; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 78; 86pp; English.
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Misc-difference 1..44
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 AA;
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                                                                                                Modified GLA
                                                                                                                                                                  Homo sapiens
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                                            AAY18297;
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                                                                                                                                           therapy.
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Matches
AAY18297
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide with modified gamma-carboxyglutamic for treating clotting disorders
                                                                                                                                                                                                                                                                                                   GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
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                                                                                                            Modified GLA domain of vitamin K-dependent protein.
                                                                                                1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                           Score 170; DB 20;
Pred. No. 4.2e-21;
1; Mismatches 1;
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Pred. No. 9.1e-21;
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                                                                                                                                                                                          AAY18307 standard; peptide; 44
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95.5%;
                                            86.3%;
95.5%;
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                                           Query Match 86.3
Best Local Similarity 95.5
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vitamin K-dependent acid domain, useful
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Best Local Similarity
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                   44 AA;
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Synthetic.
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                                                                                                                                                                                                                     AAY18307;
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                  Sequence
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This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the affinity as compared to the native protein which has enhanced membrane binding affinity as compared to the native protein.
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                                                                                                                                                                                                                                                                                                                                                                                       1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                               Score 168; DB 20;
Pred. No. 9.1e-21;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY18309 standard; peptide; 44
                                                                                                                                                                                                                                                                    85.3%;
95.5%;
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RESULT 14

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Synthetic.

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This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                               /note- "Xaa- gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 79-80; 86pp; English.
Location/Qualifiers Misc-difference 1..44
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Search completed: May 15, 2003, 13:27:16 Job time : 36 secs

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Gaps

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Query Match 81.2%; Score 160; DB 20; Length 44; Best Local Similarity 93.2%; Pred. No. 2e-19; Matches 41; Conservative 0; Mismatches 3; Indels

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein – protein search, using sw model

Run on:

May 15, 2003, 13:26:07 ; Search time 18 Seconds (without alignments) 234.995 Million cell updates/sec

1 ANSFLXXLRQGSLXRXCIXX.....XXAKXIFEDVDDTLAFWSKH 44 SEQIDI_MOD Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
3: pir2:*
: pir3:*
: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	protein C (activat	υ	υ	U	10	coagulation factor	coagulation factor	coagulation factor	coagulation factor	73	thrombin (EC 3.4.2	coagulation factor	coagulation factor	plasma protein S p	plasma protein S p	thrombin (EC 3.4.2	plasma protein S -	coagulation factor	coagulation factor	coagulation factor	prote	protein S		coagulation factor	thrombin (EC 3.4.2	plasma protein S p			growth arrest-spec
SUMMARIES			0	4					7		1	7			4			6	1	6			3							6
SU	QI :	KXHU	JX0210	S18994	KXBO	EXRT	EXBO	EXHO	146932	KFHU7	S10511	A35827	EXCH	KFB07	S53434	KXHUS	TBHO	S38819	A30351	JQ0419	KFHU	KXBOS	S53433	KXRTS	KFBO	TBBO	KXMSS	KXBOZ	KXHU2	A48089
	DB	-	-	-	Н	ч		-	~	-	~	~	-	Н	N	Н	7	~	-	7	-	-	7	-	-	Н	Н	-	Н	7
	Query Match Length	461	461	461	456	482	492	488	443	466	617	618	475	407	642	9/9	622	646	452	459	461	675	642	675	416	625	675	396	422	673
đ	Query Match	81.2	71.1	70.6	61.9	58.4	57.9	55.8	51.3	50.3	43.9	43.9	43.7	43.1	43.1	43.1	42.6	41.1	40.6	40.6	40.6	40.6	39.6	39.6	37.1	36.5	36.0	35.3	33.5	33.0
	Score	160	. 140	139	122	115	114	110	101	66		86.5	98		82		84	81		. 80		80	78	78	73	72	71	69.5	S	65
	Result No.	-	7	e	4	ស	9	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	. 52	36	27	28	53

growth potentiatin growth arrest-spec	probable MAP kinas probable MAP kinas probable MAP kinas		hypothetical prote ammonium transport mitogen-activated	VSG expression sit protein-tyrosine k	tyrosine kinase re type II site-speci
155476 B48089	D84859 · C96575 G96763	T40556 T02367 T58375	T25948 E82918 T39306	D32433 A48999	333/2/ JC1189 NDECR5
0.0	000	777	000	777	177
674 678	594 603 576	606 1684 1363	323 510 422	1235	182 245
ĸΟ	r.r.u	0.40	6664	44.	16.6
32	27	25	24.6	777	333
64 63	56.5 53.5 53.5	53 80 80	4 8	4 4 8 8 8 8	
30 31	0 0 0 0 0 4	35 36 37	8 8 8 9 0 0	444	444

ALIGNMENTS

	RESULT 1 KXHU Protein C (activated) (EC 3.4.21.69) precursor - human N.Alternate names: autoprothrombin IIA; plasma protein C C; Species: Homo sapiens (man) C; Date: 17-Mar-1987 #text_change 16-Jul-1999 C: Acression: a23331: a25426. a31781: a231781.
-	RiPoster, D.C.; Yoshitake, S.; Davie, P.V.; NOOSE,
	A; Residues: 1.461 <pre>A; Residues: 1.461 <pre>CPOSI></pre> A; Cross references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334 R;Plutzky, J; Hoskins, J.A.; Long, G.L.; Crabtree, G.R. Proc. Natl. Acad. Sci. U.S.A. 83, 546-556, 1986 A.Title: Evolution and organization of the human protein C gene. A; Reference number: A25426; MUID:86120978; PMID:3511471 A; Accession: A25426</pre>
Ņ.	A; Molecule type: DNA A; Residues: 1.445, 'L', 446-461 < PLU> A; Residues: 1.445, 'L', 446-461 < PLU> A; Residues: 1.445, 'L', 446-461 < PLU> A; Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332 R; Foster, D.; Davie, E.W. Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984 A; Title: Characterization of a cDNA coding for human protein C. A; Reference number: A21781; MUID:84272714; PMID:6589623
	A. MOLJEULE LYPE, MENNA A. Rossidues: 'Q','107-461 <fos2> A.Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323 A.Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323 Nucleic Acids Res. 13, 5233-5247, 1995 A.Title: The structure and evolution of a 461 amino acid human protein C precursor an A.Accession: A23789; MUID:85269639; PMID:2991859 A.Accession: A23789 A.Molecule type: mRNA</fos2>
	A.Residues: 1-461 <bec> A.Residues: 1-461 <bec> A.Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120 R.Miletlch, J.P.; Broze Jr., G.J. J. Biol. Chem. 265, 11397-11404, 1990</bec></bec>
	A;Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation A;Reference number: A44605; WIDD:90239034; PMID:1694179 A;Contents: annotation; Carbohydrate binding sites; activation peptide A;Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is R;Harris, R.J.; Ling, V.T.; Spellman, M.W. Biol. Chem. 267, 5102-5107, 1992 A;Title: O-linked fucose is present in the first epidermal growth factor domain of fa A;Reference number: A44606; MUID:92184750; PMID:1544894 A;Contents: annotation; beta-hydroxyaspartic acid C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinsse that ivation of factor Va is strongly enhanced by complexing with protein S. Protein C als

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Conservative
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A;Molecule type: mRNA
A;Residues: 1-461 <OKA2>
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A; Residues: 1-456 <LON>
R; Fernlund, P.; Stenflo,
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Matches 26; Conserv
                                                                                    Similarity
                                        Query Match
Best Local Simi
Matches 26;
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                                                                                                                                                                                               A Map position: 2413-2421
A; Introns: 2417, 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A; Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology
C; Keywords: anticoagulant; Deta-hydroxyaspartic acid; blood coagulation; calcium binding
F; 1-37/Domain: signal sequence #status predicted <SIG>
F; 37-86/Domain: Gla domain homology <GLA>
F; 33-42/Domain: propeptide #status predicted <PRO>
F; 33-4197/Product: protein C light chain #status predicted <LCH>
F; 92-131/Domain: EGF homology <EGL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;140-175/Domain: EGF homology <EG2>
F;140-175/Domain: EGF homology <EG2>
F;200-461/Product: protein C heavy chain #status predicted <HCH>
F;200-461/Product: protein C heavy chain #status experimental <APT>
F;212-445/Domain: activation peptide #status experimental <APT>
F;212-445/Domain: activation peptide #status experimental cacid (Glu) #status experimental E;39-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D F;106-111/Disulfide bonds: #status predicted
F;110/Malnding site: carbohydrate (Thr) (covalent) #status absent
F;139,290,355/Binding site: carbohydrate (Apn) (covalent) #status experimental F;212/Cleavage site: Arg-Leu (thrombin) #status experimental F;212/Cleavage site: Arg-Leu (thrombin) #status experimental F;213,200,355/Ative site: Arg-Leu (thrombin) #status experimental F;23,299,402/Active site: Hist. Asp, Ser #status predicted
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F;47,48,55,57,60,61,66,67,70,76,Modified site: gamma-carboxyglutamic acid (Glu) #status F;12/Modified site: erythro-beten-hydroxyaspartic acid (Asp) #status predicted F;121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat F;214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted F;233,299,402/Active site: His, Asp, Ser #status predicted
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F; 27-85-Domain: Gla domain homology <GLA>
F; 34-41/Domain: propeptide #status predicted <PRO>
F; 42-196-Product: protein C #status predicted <PRO>
F; 42-196-Domain: light chain #status predicted <PRO>
F; 42-196-Domain: EGF homology <EGI>
F; 91-130/Domain: EGF homology <EGI>
C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
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;199-461/Domain: heavy chain #status predicted <PCH>
;199-211/Domain: activation peptide #status predicted <ACT>
;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VII>
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N;Alternate names: vitamin K dependent serine proteinase
C;Species: Mus musculus (house mouse)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
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R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh,
J. Biochem. 111, 491-495, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.2%; Score 160; DB 1; Length 461; llarity 70.5%; Pred. No. 8.8e-18; Conservative 2; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:120317; OMIM:176860
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Best Local Similarity
Matches 31; Conserv
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F;91-130/Domain: EGF homology <EG2>
F;139-174/Domain: EGF homology <EG2>
F;213-445/Domain: trypsin homology <TRY>
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat F;12/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;112/1-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #sF;121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #sF;215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol C;Reywords: befarhydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase F;1-37-95/Domain: signal sequence #status predicted <SIG>F;27-85/Domain: gla domain homology <GLA>F;37-42/Domain: propeptide #status predicted <PRO>F;33-42/Domain: protein C #status predicted <PRO>F;43-46/Product: protein C #status predicted <PRC>
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Sabelia: 10.5ep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C;Accession: S18994; S.24312
A;Description: The CDNA cloninig and mRNA expression of rat protein C.
A;Reference number: S18994
A;Roccession: S18994
A;References: EMBL;Reference References: EMBL;Reference Reference Ref
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NyAlternate names: autoprothrombin IIA; plasma protein C C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30.Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26520; A18385; A3886; A09528
R;Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A;Reference number: A26250; MUID:85014826; PMID:6091100
                                                                                                                      Gaps
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           Length 461;
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                                                                                                                      11; Indels
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Blochim. Biophys. Acta 1131, 329-332, 1992
A;Title: The cDNA cloning and mRNA expression of rat protein
A;Reference number: S24312; MUID:92329550; PMID:1627650
A;Accession: S24312
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                                                                                                                                                                                                                                                                                                        42 ANSFLEEMRPGSLERECMEEICDFEEAQEIFONVEDTLAFWIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 ANSFLEEVRAGSLERECMEEICDFEEAQEIFONVEDTLAFWIKY
                                                                                                                                                                                                                                      1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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Score 140; DB 1;
Pred. No. 1.5e-14;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.1e 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.6%; Score 139;
     71.1%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 59.1%;
Conservative
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Fil83-231/Domain: activation peptide *status predicted <APTY Fil83-231/Domain: activation peptide *status predicted <APTY Fil22-462/Product: coagulation factor Xa heavy chain *status.predicted <ACTY Fil23-460/Domain: trypsin homology <TRYY Fil23-460/Domain: trypsin homology <TRYY Fil64-47.54.56.59,60.65,66.69,72.79/Modified site: gamma-carboxyglutamic acid (Glu) *spir.57-62.90-101.95-110,112-121,129-140,136-149,151-164,172-340.238-233,259-275,388-402 Fil37/Modified site: erythro-beta-hydroxyaspartic acid (Asp) *status predicted Fil208/Binding site: carbohydrate (Asn) (covalent) *status predicted Fil218/Binding site: carbohydrate (Thr) (covalent) *status predicted Fil218/Binding site: arbohydrate (Asn) (covalent) *status predicted Fil213-232/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) *ssi274,320,417/Active site: His, Asp, Ser *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A: Pathway: blood coagulation factor X; EGF homology; Gla domain homology; trypsin homology blood coagulation factor X; EGF homology; Gla domain homology; trypsin homology categories that a propertie acid; blood coagulation; calcium binding; carboxyglu F: 1-23/Domain: signal sequence status predicted <SIG> F: 24-40/Domain: propeptide status predicted <PRO> F: 25-84/Domain: dia domain homology <GLA> F: 25-84/Domain: Gla domain homology <GLA> F: 30-121/Domain: EGF homology <EGL> F: 30-121/Domain: EGF homology <EGL> F: 30-121/Domain: EGF homology <EGL> F: 383-482/Product: coagulation factor X heavy chain status predicted <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: catalyzes the proteclytic activation of prothrombin to thrombin in the
                                                                                              A.Residues: 1-482 - CSTA1.
A.Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A.Note: submitted to the EMBL Data Library, June 1994
A.Note: neither the complete nucleic acid sequence nor the complete translation are 8 R.Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A.Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A.Reference number: JC4670; MUID:96194815; PMID:8647460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-482 <STA2>
A; Residues: 1-482 = EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A; Experimental source: Cos-1 cell
R; Enjyoji, K.; Miyazaki, K.; Kato, H.
J. Blochen. 109, 890-898, 1991
J; A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat A; Reference number: PS0190; MUID:92041742; PMID:1718949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 133-186, 'X', 188-207 < ENJ2>
A; Residues: 133-186, 'X', 188-207 < ENJ2>
Eur. J. Haematol. 52, 162-168, 1994
A; Title: Analysis of the partial nucleotide sequences and deduced primary structures
A; Reference number: 146196; MUID:94222160; PMID:8168596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 295-383,'C',385-455 <MUR>
A;Cross-references: GB:D21215; NID:9415309; PIDN:BAA04756.1; PID:9455396
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ANSFFEEIKKGNLERECVEEICSFEEAREVFEDNEKTTEFWNKY
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ilarity 43.2%; Pred. No. 1.7e-10;
Conservative 10; Mismatches 15:
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A; Residues: 41-58, 'X', 60-65 <ENJ1>
A; Accession: PS0190
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Best Local Similarity
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A. Residues: 197-454, 'PV' - CSTE>

A. Residues: 197-454, 'PV' - CSTE>

B. Residues: 197-454, 'PV' - CSTE>

J. Babault. L. E., Esmon, C.T.

J. Biol. Chem. 238, 5548-5553, 1983

A. Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F. A. Reference number: A37541; MUID: 83.213513; PMID: 6304092

A. Reference number: A37541; MUID: 83.213513; PMID: 63.04092

B. Johnson, A. E.; Esmon, N. L.; Laue, T. M.; Esmon, C.T.

J. Biol. Chem. 258, 5554-5560, 1983

A. Title: Structural changes required for activation of protein C are induced by Ca2+ bin A; Reference number: A37542; MUID: 83.213514; PMID: 6406503

A. Contents: annotation; activation; calcium binding
C. Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is oblin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacticy comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stracognition of the thrombin-thrombomodulin complex.

C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C;Superfamily: coagulation factor X; EgF homology; Gla domain homology; trypsin homology C;Reywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding F;1-29/Domain: signal sequence (fragment) *status predicted <SIG> *SIG> *SIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F.137-172/Domain: EGF homology /Fig2>
F.197-20.00main: EGF homology /Fig2>
F.197-20.00main: activation peptide *status experimental <hC>/Fig20-40.00main: activation peptide *status experimental <a href="https://www.new.org/">www.new.org/</a>
F.211-440/Domain: activation peptide *status experimental <a href="https://www.new.org/">F:211-440/Domain: activation peptide *status</a>
F.211-440/Domain: trypsin homology <a href="https://www.new.org/">www.new.org/</a>
F.212-440/Domain: trypsin homology <a href="https://www.new.org/">www.new.org/</a>
F.310/Modified site: activation displaymente (Asp) #status predicted
F.119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: *stat
F.3156,289,397/Active site: His, Asp, Ser *status predicted
F.356/Binding site: carbohydrate (Asn) (covalent) *status predicted
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C;Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
C;Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
C;Datession: S49075; JG4670; PS0191; PS0190; I62745
R;Stanton, C;Ross, P;Hutson, S;Wallin, R.
Thromb. Res. 80, 63-73, 1995
A;Title: Evidence for competition between vitamin K-dependent clotting factors for intra A;Reference number: A58498; MUID:96093366; PMID:8578539
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A; Residues: 40-194 < FER>
A; Residues: 40-194 < FER>
A; Rote: 82-Lys was also found
B; Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A; Title: beta-Hydroxyasparitc acid in vitamin K-dependent protein C.
A; Reference number: A19316; MUD: 83169769; PMID: 6572939
A; Contents: annotation; revision to residue 110
R; Stenflo., J.; Fernlund, P.
J. Blol. Chem. 277, 12180-12190, 1982
A; Title: Amino acid sequence of the heavy chain of bovine protein C.
A; Reference number: A18386; MUD: 83007326; PMID: 6896877
J. Biol. Chem. 257, 12170-12179, 1982
A;Title: Amino acid sequence of the light chain of bovine protein C. A;Reference number: A18385; MUID:83007325; PMID:6896876
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Best Local Similarity 50.0°
Matches 21; Conservative
                                                                                                                                                                           A; Accession: A18385
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A Pathway: Diood coagulation for the coagulation of Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology c; Superfamily: coagulation factor x light chain #status experimental circh> F; 16-40/Domain: signal sequence #status predicted <PRO> F; 25-84/Domain: Dia domain homology cGLA> F; 21-44/Domain: Dia domain homology cGLA> F; 21-44/Domain: EGF homology cEGL> F; 21-44/Domain: EGF homology cEGL> F; 21-44/Domain: EGF homology cEGL> F; 234-44/Domain: EGF homology cEGL> F; 234-46/Domain: EGF homology cEGL> F; 235-46/Domain: EGF homology cEGL> F; 231-418/ACLEavage site: Arg-Ile (Coagulation factor IXa, Coagulation factor VIIa) #S; 235-235, 231, 418/ACLEavage site: His, Asp, Ser #status predicted
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A; Molecule type: mRNA
A; Residues: 1-488 cMES>
A; Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390
A; Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390
B; Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, B.W.
J. Biol. Chem. 267, 7395-7401, 1992
A; Title: Liver-specific expression of the gene coding for human factor X, a blood coa A; Reference number: A42485; MUID:92218390; PMID:1313796
                                                                                      catalyzes the proteolytic activation of prothrombin to thrombin in the
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C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 # sequence_revision 02-May-1994 #text_change 08-Dec-2000
C;Date: 15-Nov-1984 # sequence_revision 02-May-1994 #text_change 08-Dec-2000
C;Accession: A4478; J00917; A2285; A2285; A22208; A21284; A20362; S39415; I54051;
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Blochemistry 25; 5098-5102, 1986
A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization
A;Reference number: A24478; MUID:87026600; PMID:3768336
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A; Residues: 1-488 <-LEY>
A; Cross-references: GB:L29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; PID:g182831
A; Cross-references: GB:L29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; PID:g182831
Gene 99, 291-294, 1991
A; Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human
A; Reference number: JQ0917; MUID:91216473; PMID:1902434
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A; Residues: 1-15 < MIA>
A; Residues: 1-15 < MIA>
A; Experimental Source: liver
A; Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIP:93787)
R; Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
R; Kaul, S.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
A; Title: Isolation and characterization of human blood-coagulation factor A; Reference number: A25853; MUID:86221713; PMID:3011603
A; Accession: A25853.
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Pred. No. 2.5e-10;
8; Mismatches 16; Indels
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A;Residues: 19-284,'E',289-488 <KAU>
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45.5%;
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Best Local Similarity 45.5
Matches 20; Conservative
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R/Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.

Biol. Chem. 259, 5705-5710, 1984

A/TILE: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic A/Reference number: A38024; MUID:84185716; PMID:6546930

A/Contents: annotation; calcium binding

A/Contents: annotation; calcium binding

R/Morita, T.; Jackson, C.M.

J. Biol. Chem. 261, 4008-4014, 1986

A/Reference number: A38025; MUID:86140210; PMID:3949800

A/Contents: annotation; sulfate binding

A/Contents: Cactor Xa converts prothrombin to thrombin during blood clotting.

C/Comment: Factor Xa converts prothrombin from a single-chain precursor by the excision of tw

C/Comment: The two chains are formed from a single-chain precursor by the excision of tw

C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
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A; Wolecule type: protein
A; Residues: 183-292,294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <TA; A; Residues: 183-292,294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <TA; Note: carbohydrate binding sites and disulfide bonds were determined
R; Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
J. Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A; Reference number: A34412; MUID:89380326; PMID:2789221
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A; Residues: 183-196;199-209;216-233 <INO>
A; Residues: 183-196;199-209;216-233 <INO>
A; Residues: 183-196;199-209;216-233 <INO>
A; Residues: 183-196;199-209;216-233 <INO>
A; Residues: 183-196;199-4903, 1972
B; Molecular to the set of the
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C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C;Accession: A22867; A14997; A12030; A34412; S39414; A00925
R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing A; Acference number: A22867; MUID:84247315; PMID:6330671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 41-102, W. 104-180 < ENF>
A; Residues: 41-102, W. 104-180 < ENF>
B; McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. B.A.; Fujikawa, K.; Kisiel, W.
Biochem. B.A.; Fujikawa, R.; Beta-hydroxyaspartic acid in the vitamin K-dependent blood of R; Reference number: A20244; MUID: 83308813; PMID: 6688526
A; Contents: annotation; revision to residue 103
A; Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad Sci. U.S.A. 72, 3082-3086, 1975
A; Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A; Reference number: A12030; MUID: 76053069; PMID: 1059093
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                                                                                                                                                                                                                                                                                                                                                          ; Molecule type: mRNA
; Residues: 1-487 <FUN>
; Cross-references: GB: X00673; NID:g192; PIDN:CAA25286.1; PID:g193
; Enfletd, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
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A; Residues: 85-126 <PER>
A; Note: beta-hydroxyaspartic acid site
R; Inoue, K.; Morita, T.
Bur. J. Biochem. 218, 153-163, 1993
A; Title: Identification of O-linked oligosaccharide chai
A; Reference number: $39414; MUID:94062825; PMID:8243461
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A;Map position: 13q34
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Gaps

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Length 492;

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C.Species: Homo sapiens (man)
C.Species: Homo (man)

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C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F; 24-83/Domain: Gla domain homology < GLA>
F; 24-83/Domain: EGF homology < GEL>
F; 130-166/Domain: EGF homology < EGL>
F; 130-166/Domain: trypsin homology < TRY>
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A; Readules: 1-466 <001A
A; Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
A; Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart
Proc. Natl. Acad. Sci. U.S., B3; 2412-2416, 1986
Prille: Characterization of a cDNA coding for human factor VII.
A; Reference number: A23819; MUID:86205965; PMID:3486420
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R;Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen,
Biochemistry 27, 7785-7793, 1988
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A;Reference number: A90539; MUID:89088153; PMID:3264725
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                F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;199,211/Mainding site: carbohydrate (Thr) (covalent) #status experimental F;221,231/Mainding site: carbohydrate (Asn) (covalent) #status experimental F;234-235/Cleavage site: Arg-ile (coagulation factor IXa, coagulation factor VIIa) F;276,322,419/Active site: His, Asp, Ser #status experimental
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C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C;Accession: 14693-1897
Thromb. Res. 69, 231-238, 1993
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Pred. No. 1.1e-09;
9; Mismatches 16
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-443 <BRO>
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Best Local Similarity 43.2%;
Matches 19; Conservative
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Best Local Similarity 46.3%
Watches 19; Conservative
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A; Residues: 1-466 <HAG>
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R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla
J. Mol. Biol. 232, 947-966, 1993
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A:Reference number: A49458; MUID:93560277; PMID:8355279
A:Contents: annotation: X-ray crystallography, 2.2 angstroms
C;Comment: The two chains held together by one disulfide bond are formed from a single-c
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;129-164/Domain: EGF homology <EG2>
F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-488/Product: coagulation peptide #status experimental <ACT>
F;235-462/Domain: activation peptide #status experimental <ACT>
F;235-462/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,97,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;57-62/Disulfide bonds: #status predicted
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443,
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A; Mesiduces: 183-234 <INO.
A; Notes: glycosylation sites
A; Note: glycosylation sites
A; Note: identification and characterization of beta-hydroxyaspartic acid
B; Jagadesswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, G.
Gene 84, 517-519, 1989
A; Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A; Reference number: 154051; MUID:90128299; PMID:2612918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins
Biochemistry 22, 2875-2884, 1983
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A:Reference number: A20362; MUID:83257207; PMID:6871167
                                                                                                                                                                           coding for human blood coagulat:
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A;Readdues: 41-179 4KCMP>
A;Readdues: 41-179 4KCMP>
R;Inoue, K; Morita, T.

Eur. J. Blochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides
A;Reference number: $39414; MUID:94062825; PMID:8243461
A;Accession: $339415
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 13-441, S', 443-488 <PUN>
A; Cross-references: GB: K03194; NID: 9182840; PIDN: AAA52490.1; PID: 9182841
A; Leytus, S.P.; Chung, D.W.; K1siel, W.; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
A; Title: Characterization of a cDNA coding for human factor X.
A; Reference number: A21284; MUID: 84222026; PMID: 5587384
                PIDN: AAA51984.1; PID:9180336
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A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:M22613; NID:g180335; PIDN:AAA5198
R;Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A;Title: Characterization of an almost full-length cDNA
A;Reference number: A22208; WUID:85216545; PMID:2582420
A;Accession: A22208
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A;Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A;Note: deficiency of this factor causes Stuart disease
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A;Residues: 13-284,'E',289-488 <LE2>
A;Cross-references: GB:K01886
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A. Residues: 384-618, 'E' < CANN>
A. Cross references: GB: M81394
C. Suberfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C. Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; h
F: 1-24-70 momain: signal sequence * status predicted < RNO>
F: 28-88/Domain: propeptide * status predicted < RNO>
F: 28-88/Domain: kringle homology < CRN>
F: 46-610/Domain: kringle homology < CRN>
F: 361-610/Domain: kringle homology < CRN>
F: 361-66, 51.58, 60, 63.64, 69, 70, 73.76/Modified site: gamma-carboxyglutamic acid (Glu) * status F: 61-66, 91-104, 109-187, 130-170, 188-182, 233, 236-276, 264-288, 333-479, 388-404, 533-54
F: 403, 459, 565/Active site: His, Asp, Ser * status predicted
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A; Residues: 1-618 < DEGS
A; Residues: 1-618 < DEGS
A; Experimentes: GB: X52308; NID: 953813; PIDN: CAA36548.1; PID: 953814
A; Experimental source: strain G7BL/6
A; Note: the data were obtained from females resulting from the cross of M. domesticus
R; Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and
A; Reference number: A42696; MUID: 92212913; PMID: 1557383
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                                                  A Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Reference number: A42696; MUD:9212913; PMID:1557383
A;Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Bate: 14-Dec-1990 #text_change 03-May-2002
C;Accession: A35827, A42696; S12081
R;Degen, S.J.F.; Schefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, DNA cell Biol. 9, 487-488, 1990
A;Title: Characterization of the cDNA coding for mouse prothrombin and localization A;Reference number: A35827, MUID:91025551; PMID:2222810
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Pred. No. 8.5e-06;
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A.; Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a A; Reference number: A40529; WUID:91204011; PMID:1904059
A.; Contents: annotation; carbohydrate binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Persson, E.; Petersen, L.C.
Eur. J. Blochem. 234, 293-300, 1995
A.Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A.Reference number: $63524; MUID:96096752; PMID:8529655
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A; Residues: 1-617 ADIN-
A; Residues: 1-617 ADIN-
A; Cross-references: EMBL: X52835; NID:956969; PIDN:CAA37017.1; PID:956970
A; Cross-references: EMBL: X52835; NID:956969; DIDN:CAA37017.1; PID:956970
E; Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A; Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A; Reference number: A60576; MUID:90091942; PMID:2293980
A; Accession: A60576
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C;Dacesion: S10511; A0576; B42696
C;Dacesion: S10511; A0576; B42696
C;Accesion: S10511; A0576; B42696
C;Accesion: S10511; A0776; B42696
C;Accesion: S10511; Mulard, D.
Nucleic Acids Res. 18, 4251, 1990
A;Title: CDNA sequence of rat prothrombin.
A;Reference number: S10511; MulD:90332426; PMID:2377469
A;Reference number: S10511.
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A;Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
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4; Mismatches 17; Indels
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Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.3%; Score 99;
ilarity 48.8%; Pred. No. (
Conservative 4; Mismatc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GDB:119897; OMIM:227500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombin (EC 3.4.21.5) precursor - rat
A; Molecule type: protein
A; Residues: 213-466 (TH2>
R; Bjoern, S.; Roston
J, Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
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Best Local Similarity
Matches 20; Conserv
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Length

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J. Blochem. 104, 867-868, 1988

A; Thle: A new trisaccharide sugar chain linked to a serine residue in bovine blood c.; Na. A; Reference number: A44556; MUID:89213999; PMID:3149637

A; Reference number: and location of covalently bound carbohydrate

C; Function:
A; Reterence and location of covalently bound carbohydrate

C; Superfamily: coagulation extrinate pathway
C; Superfamily: coagulation factor X; Esf homology; Captom and tissue factor
C; Superfamily: coagulation factor Xis light chain *status experimental chain
C; Superfamily: coagulation factor VIIa light chain *status experimental chain
C; Superfamily: Captomain: GIR domain homology (fragment) collection factor MAID
C; Superfamily: Captomain: EGF homology cEGID>
F; 13-40//Product: coagulation factor VIIa heavy chain *status experimental chain
F; 50-81/Domain: EGF homology cEGID>
F; 51-127/Domain: EGF homology cEG
                                                                                                                      A;Molecule type: protein
A;Residues: 1-407 <TAKS
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. B.A.; Fujikawa, K.; Kisiel, W.
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A;Reference number: A20274; MUID:83308813; PMID:6688526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 58-62, 'X', 64-68 <MCM>
A;Residues: the residue designated 'X' was determined to be hydroxyaspartic acid
A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid
B;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanag
J. Blochem. 104, 867-868, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat E;1-51/Domain: Gla domain homology (fragment) <GLA>
E;1-57/Domain: signal sequence (fragment) #status predicted <SIG>
E;8-642/Product: plasma protein S #status predicted <MAT>
E;8-642/Product: plasma protein S #status predicted <MAT>
F;87-120/Domain: EGF homology <EG1>
E;127-165/Domain: EGF homology <EG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Macaca mulatta (rheaus macaque) (c.Species: Macaca mulatta (rheaus macaque) (r.Species: Macaca mulatta (rheaus macaque) (c.Species: Macaca mulatta (rheaus macaque) (c.Species: Macacasion) (s.Ssa) (s.Ssa)
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A; Reference number: A31979; MUID:89008362; PMID:3049594 A; Accession: A31979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANGFLEELLPGSLERECREELCSFEEAHEIFRNEERTROFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 85; DB 1;
Pred. No. 9.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 43.9%;
Matches 18; Conservative
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A; Residues: 1-642 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: C20274
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F;46.47,54,56,59,60,65,66.69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #8
F;46.47,54,56,59,50,59,60,65,66.89,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #8
F;57-66,90-101,95-110,112-121,1221,129-140,136-152,154-167,175-348,247-252,567-283,396-410,42
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;282,328,425/Active site: His, Asp, Ser #status predicted
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R;Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
R;BSL Lett. 296, 274-278, 1992
A;Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsit A;Reference number: S20380; MUID:92164779; PMID:1537403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coagulation factor Xa (EC 3.4.21.6) precursor - chicken

Nathernate names: virus-activating proteinase
C; Species: Gallus gallus (chicken)
C; Date: 12-Peb-1993 #sequence_revision 07-Peb-1997 #text_change 16-Jul-1999
C; Date: 12-Peb-1993 #sequence_revision 07-Peb-1997 #text_change 16-Jul-1999
C; Date: 12-Peb-1993 #sequence_revision 07-Peb-1997 #text_change 16-Jul-1999
R; Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
FEBS Lett. 283, 281-285, 1991
A; File: Primary structure of the virus activating protease from chick embryo. Its ident
A; Reference number: S15838 MUID:91257322; PMID:2044767
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F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F:186-240/Domain: activation peptide #status predicted <APT>
F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
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C; Species: Bos primigenius taurus (cattle)
C; Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C; Accession: A31979; C20274
R; Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, J. Blol. Chem. 263, 14868-14877, 1988
A; Title: Bovine factor VII. Its purification and complete amino acid sequence.
                                                                       Gaps
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                                                                 Indels
                                                                                                                                                                                                                                                                                      44 ANSCFLEELRKGNLERECVEEQCSYEEAFEALESPODTDVFWAKY 88
                                                                                                                                                                                 ANS-FLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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Pred. No. 7.8e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-475 <SUZ>
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A;Residues: 241-246, x',248-251, x',253-261 <GOT>
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           Pred.
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                                                                 Conservative
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A; Residues: 41-55 <GO2>
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seqidl_mod,rpr

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Appending a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage d c) Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat C; Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat C; Keywords: beta-hydroxyaspartic acid; blood coagulation; car F; 1-24/Domain: signal sequence #status predicted <RRO> F; 25-41/Domain: propeptide #status predicted <RRO> F; 26-85/Domain: gla domain homology <GLA> F; 26-85/Domain: EGF homology <GLA> F; 21-154/Domain: EGF homology <EGS> F; 101-154/Domain: EGF homology <EGS> F; 101-199/Domain: EGF homology <EGS> F; 247-282/Domain: EGF homology <EGS> F; 248/Domain: EGF homology <EGS F; 248/Domain
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F;47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;58-63,88-113,121-114,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-24
F;58-63,88-113,121-114,270-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,186-184,1
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A.Introns: 26/1; 78/3; 87/1; 116/1; 157/1; 201/1; 243/1; 283/3; 322/2; 385/3; 441/3;
C.Complex: in plasma forms a complex with C4b binding protein
                      A;Title: Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus sequences for A;Reference number: S02424; MUID:88005138; PMID:2820795
                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: Y00692; NID: 936578; PIDN: CAA68687.1; PID: 936579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:120721; OMIM:176880
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Job time : 19 secs
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38.6%;
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Best Local Similarity 38.6%
Matches 17; Conservative
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A; Residues: 1-676 <PL2>
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                                                                                                                                                                              A; Accession: S02424
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Proc. Natl. Acad. Sci. U.S.A. 84, 349-353, 1987
Proc. Inatl. Acad. Sci. U.S.A. 84, 349-353, 1987
A;Title: Cloning and characterization of human liver cDNA encoding a protein S precursor A;Reference number: A26157; MUID:87092407; PMID:3467362
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A; Residues: 1-10, 'P',12-25,'L',27-676 <HOS>
A; Residues: 1-10, 'P',12-25,'L',27-676 <HOS>
B; Richards-rences: 1-10, 'P',12-25,'L',27-676 <HOS>
B; Lundwarll, A.; Dackowski, W.; Cohen, E.; Shaffer, M.; Mahr, A.; Dahlback, B.; Stenflo, Proc. Natl. Acad. Sci. U.S.A. 83, 6716-6720, 1986
A; Title: Isolation and sequence of the CNNA for human protein S, a regulator of blood contains and sequence of the CNNA for human protein S, a regulator of blood contains at the CNNA for human protein S, a regulator of blood contains at the CNNA for human protein S, a regulator of blood contains at the CNNA for human protein S, a regulator of blood contains at the CNNA for human protein S, a regulator of blood contains at the CNNA for human protein S, a regulator of blood contains at the CNNA for human protein S, a regulator of blood contains at the CNNA for human protein S, a regulator of blood contains at the CNNA for human protein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of blood contains at the CNNA for human brotein S, a regulator of the CNNA for human brotein S, a regulator of the CNNA for human brotein S, a regulator of the CNNA for human brotein S, a regulator 
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A;Residues: 27-220, L', 222-262, 'H', 264-344,'Y', 346-676 <LUN>
A;Cross-references: GB:M14338; NID:9190448; PIDN:AAA60181.1; PID:9190449
A;Note: part of this sequence, including the amino end of the mature protein, was determ
R;Edenbrandt, C.M.; Lundwall, A.; Wydro, R.; Stenflo, J.
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A;Title: Two genes homologous with human protein S CDNA are located on chromosome 3. A;Reference number: A60903; MUID:88170564; PMID:2895503
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A;Note: the authors translated the codon TTT for residue 26 as Leu
K.P.Loos van Amstel, H.K.; Reitsma, P.H.; van der Logt, C.P.E.; Bertina, R.M.
Biochemistry 29, 7853-7861, 1990
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A;Residues: 351.676 cPLO>
R:Ploos van Amstel, H.K.; van der Zanden, A.L.; Reitsma, P.H.; Bertina, R.M.
FEBS Lett. 222, 186-190, 1987
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| Species: Homo sapiens (man)
| Date: 21-Sep-1990 #sequence_revision 26-Jan-1996 #text_change 16-Jul-1999
| Accession: A35610; A35611; A26157; A25891; A35612; A60903; S02424; S09519
| Schmidel, D.K.; Tatro, A.V.; Phelps, L.G.; Tomczak, J.A.; Long, G.L.
| Lochemistry 29, 7845-7852, 1990
| State: Organization of the human protein S genes.
| Reference number: A35610; MUID:91084444; PMID:2148110
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F;171-207/Domain: EGF homology <EG3>
F;213-248/Domain: EGF homology <EG4>
F;281-633/Domain: sex hormone-binding globulin homology <SHB>
F;281-444/Domain: laminin G repeat homology <LGR>
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; Pred. No. 1.5e-05;
10; Mismatches 17
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N'Alternate names: vitamin K-dependent protein S
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38.6%;
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Best Local Similarity 38.6%
Matches 17; Conservative
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A;Residues: 1-25 <PL3>
A;Cross-references: GB:J02918
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Residues: 284-676 <EDE>
Cross-references: GB:J02919
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Length 676;

GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 15, 2003, 13:24:16 ; Search time 11 Seconds (without alignments) 165.905 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

SEGID1_MOD
197
1 ANSFLXXLRQGSLXRXCIXX.....XXAKXIFEDVDDTLAFWSKH 44

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NCBL_TaxID-9606; [1] SEQUENCE FROM N.A. MEDLINE-85270390; Pubmed-2991887; Foster D.C., Yoshitake S., Davie E.W.; Foster D.C., Yoshitake S., Davie E.W.; Foster D.C., Yoshitake S., Davie E.W.; Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985). [2] SEQUENCE FROM N.A. MEDLINE-8529639; Pubmed-2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; Proc. natl ta measenger RNA, based upon the DNA sequence of Cloned human liver cDNAs.; Nucleic Acids Res. 13:5233-5247(1985). [3] SEQUENCE FROM N.A. MEDLINE-86120976; Pubmed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Reder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Nickerson D.A.; SEQUENCE FROM N.A. Reder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Nickerson D.A.; SEQUENCE FROM N.A. RECORD C. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [5] SEQUENCE OF 106-461 FROW N.A. MEDLINE-84272714; Pubmed-589623; Foster D.C., Davie E.W.; Foster D.C., Davie E.W.; Foster D.C., Davie E.W.; ROLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; Foster D.C., Davie S.TE ASN-371. MEDLINE-9029304; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; Beta protein C is not 91ycosylated at asparagine-329; The rate translation may influence the frequency of usage at asparagine-72, 19, 19, 1810-1000. [7] [8] SEQUENCE Chem. 265:11397-11404(1990).	႘	
ESUCIENCE FROM N.A. MEDLINE-85270390; PubMed-2991887; MEDLINE-85270390; PubMed-2991887; FOSTET D.C., Yoshitake S., Davide E.W.; "The nuclectide sequence of the gene for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985). [2] SEQUENCE FROM N.A. MEDLINE-85269639; PubMed-2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its measenger RNA, based upon the DNA sequence of cloned human liver CDNAs."; Nucleic Acids Res. 13:5233-5247(1985). [3] SEQUENCE FROM N.A. MEDLINE-86120978; PubMed-3511471; Plutzky J., Boskins J.A., Long G.L., Crabtree G.R.; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. REBLINE-84273714; PubMed-6589623; FOSTER D.C., Davie E.W.; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CARBOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; PubMed-6589623; FOSTER D.C., Davie E.W.; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CABROHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; PubMed-6589623; FOSTER D.C., Davie E.W.; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CABROHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; PubMed-6590909093094; PubMed-1694179; Miletich J.P., Broce G.J. Jr.; FOSTER D.C. HOW MAY influence the frequency of usage at asparagine-xysteline sites.; J. Beta protein C is not glycosylated at tangaragine-xysteline sites.; J. Biol. Chem. 265:11397-11404(1990).	č	
REDULINE—85270390; PubMed—2991887; FOSTELNE—85270390; PubMed—2991887; FOSTELNE—85270390; PubMed—2991887; FOSTELNE—85270390; PubMed—2991887; FOSTELNE—85270390; PubMed—2991859; SEQUENCE FROM N.A. MEDLINE—85269639; PubMed—2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAs."; Nucleic Acids Res. 13:5233-5247(1985). [3] ESQUENCE FROM N.A. MEDLINE—86120978; PubMed—3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; FVOALING and organization of the human protein C gene."; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). SEQUENCE FROM N.A. NICKERSON D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE FROM N.A. SUBMITTE OF JOSTEL SCHOOL C.L., Poct C.L., Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROW N.A. MEDLINE—84272714; PubMed—5589623; FOSTEC D.C., Davie B.W.; Characterization of a cDNA coding for human protein C."; FOSTEC D.C., Davie B.W.; Characterization of a cDNA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CARBOHYDATE—LINRAGE SITE ASN-371. MEDLINE—90293094; PubMed—1694179; Miletich J.P., Broce G.J. Jr.; Beta protein C is not glycosylated at asparagine-X cysteine sites.; "Beta protein C is not glycosylated at asparagine-X cysteine sites."; "Blol. Chem. 265:11397-11404(1990).	Z.	[1]
FOSTER D.C., Yoshitake S., Davie E.W.; **Protect D.C., Yoshitake S., Davie E.W.; **The nucleotide sequence of the gene for human protein C.*; **Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985). [2] [2] SEQUENCE FROM N.A. **MEDLINE-85269639; Pubmed-2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; **The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver CDNAs.*; **Nucleic Acids Res. 13:5233-5247(1985). [3] SEQUENCE FROM N.A. **Nucleic Acids Res. 13:5233-5247(1985). [4] SEQUENCE FROM N.A. **Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [5] SEQUENCE FROM N.A. **Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Nickerson D.A.; SUBMILTE-6120714; Pubmed-5189633; FOSTER D.C., Davie E.W.; **Characterization of a cDNA coding for human protein C.*; **Froster D.C., Davie E.W.; **Characterization of a cDNA coding for human protein C.*; **Froster D.C., Davie E.W.; **Characterization of a cDNA coding for human protein C.*; **Froster D.C., Davie E.W.; ***REDLINE-62293094; Pubmed-1694179; ***Miletich J.P., Broze G.J. Jr.; ****MEDLINE-90293094; Pubmed-1694179; ****Miletich J.P., Broze G.J. Jr.; ***********************************	КЪ	SEQUENCE FROM N.A.
Foster D.C., Yoshitake S., Davie E.W.; "The nucleotide sequence of the gene for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985). [2] SEQUENCE FROM N.A. MEDLINE-85269639; PubMed-2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and ils messenger RNA, based upon the DNA sequence of cloned human liver CDNAs.; Nucleic Acids Res. 13:5233-5247(1985). SEQUENCE FROM N.A. MEDLINE-86120978; PubMed-3511471; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. REDLINE-8427214; PubMed-6589623; Foster D.C., Davie E.W.; MEDLINE-90293094; PubMed-1694179; Miletich J.P., Broze G.J. Jr.; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CARBOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; "Beta protein C is not glycosylated at asparagine-X cysteine sites."; "Beta protein C is not glycosylated at asparagine-771 (17) (1816 S.). [7] Sibil. Chem. 265:11397-11404(1990).	x	MEDLINE-85270390; PubMed-2991887;
The nucleotide sequence of the gene for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985). [2] SEQUENCE FROM N.A. MEDLINE-85269639; PubMed-2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAs."; Nucleic Acids Res. 13:523-5247(1985). [3] SEQUENCE FROM N.A. MEDLINE-86120978; PubMed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Frod ution and organization of the human protein C gene."; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. MEDLINE-84272714; PubMed-6589623; FOSTER D.C., Davie E.W.; "Characterization of a cDNA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CARBOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; PubMed-1694179; Miletich J.P., Broze G.J. Jr.; "Beta protein C is not 91ycosylated at asparagine 329. The rate it ranslation may influence the frequency of usage at asparagine-73, Biol. Chem. 265:11397-11404(1990).	≨	
Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985). [2] SEQUENCE FROM N.A. MEDLINE-65269639; Pubmed-2991859; MEDLINE-65269639; Pubmed-2991859; Packmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAs."; Nucleic Acids Res. 13:5233-5247(1985). [3] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-86120798; Pubmed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [5] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. SEQUENCE OF 106-461 FROM N.A. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [6] SEQUENCE OF 106-461 FROM N.A. MEDLINE-6427214; Pubmed-6589623; Foster D.C., Davie E.W.; "characterization of a cDNA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CARBOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; Proc. Natl. Acad. Sci. US.A. 81:4764-4770(1984). [7] Blol. Chem. 265:11397-11404(1990).	R.T	•
SEQUENCE FROM N.A. MEDLINE-85269639; PubMed-2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAS."; Nucleic Acids Res. 13:5233-5247(1985). [3] SEQUENCE FROM N.A. MEDLINE-86120978; PubMed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Froc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. HEDLINE-84272714; PubMed-6589623; SCORENCE OF 106-461 FROM N.A. HEDLINE-84272714; PubMed-6589623; Characterization of Sci. U.S.A. 81:4766-4770(1984). [6] CARBOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; PubMed-1694119; Miletich J.P., Broze G.J. Jr.; "Beta protein C is not 91ycosylated at asparagine-X cysteine sites."; "Biol. Chem. 265:11397-11404(1990).	7	Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
SEQUENCE FROM N.A. MEDLINE-85269639; PubMed-2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its measenger RNA, based upon the DNA sequence of Cloned human liver CDNAS."; Nucleic Acids Res. 13:5233-5247(1985). [3] SEQUENCE FROM N.A. MEDLINE-86120978; PubMed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Frod ution and organization of the human protein C gene."; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE O. 106-461 FROM N.A. MEDLINE-84272714; PubMed-6589623; FOSTER D.C., Davie E.W.; "Characterization of a cDNA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CARBOHYDRAFE-LINKAGE SITE ASN-371. MEDLINE-90293094; PubMed-1694179; Miletich J.P., Broze G.J. Jr.; "Beta protein C is not 91ycosylated at asparagine-X cysteine sites."; "Biol. Chem. 265:11397-11404(1990).	Z.	[2]
MEDLINE-65269639; PubMed-2991859; Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver CDNAs."; Nucleic Acids Res. 13:5233-5247(1965). [3] SEQUENCE FROM N.A. WEDLINE-66120978; PubMed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. MEDLINE-6427214; Pubmed-6589633; FOSTER D.C., Davie E.W.; "Characterization of a cDNA coding for human protein C."; Froster D.C., Davie E.W.; "Characterization of a cDNA coding for human protein C."; Froster D.C., Davie E.W.; "Characterization of a cDNA coding for human protein C."; Froster D.C., Davie E.W.; "Characterization of a cDNA coding for human protein C."; MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; Secuence of translation may influence the frequency of usage at asparagine-X cysteine sites."; J. Biol. Chem. 265:11397-11404(1990).	쬬	SEQUENCE FROM N.A.
Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAS."; Nucleic Acids Res. 13:523-5247(1985). [3] SEQUENCE FROM N.A. MEDILINE-86120978; PubMed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Evolution and organization of the human protein C gene."; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROW N.A. MEDILINE-84272714; PubMed-6589623; FOSTER D.C., Davie E.W.; "Characterization of a confactorization may influence the frequency of usage at asparagine.X cysteine sites."; "Biol. Chem. 265:11397-11404(1990).	2	
Long G.L., Long G.L., Long G.L., Long G.L., Long G.L., Long G.L., The structure and evolution of a 461 amino acid human protein C precursor and its measenger RNA, based upon the DNA sequence of cloned human liver cDNAs."; Nucleic Acids Res. 13:5233-5247(1985). [3] SEQUENCE FROW N.A. MEDLINE-86120978 PubMed=3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Yi Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROW N.A. MEDLINE-84272714; PubMed-6589623; FOSTER D.C., Davie E.W.; FOSTER D.C., Davie E.W.; FOSTER D.C., Davie E.W.; FOSTER D.C., Davie B.W.; MIDLINE-90293094; PubMed-6589623; FOSTER D.C., Davie G.J. Jr.; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). GABOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; PubMed-1694179; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Sebra procream C is not 91ycosylated at asparagine-X- Cysteine sites." J. Biol. Chem. 265:11397-11404(1990).	₹	Plutzky J., Crabtree
"The structure and evolution of a 461 anino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAS."; Nucleic Acids Res. 13:5233-5247(1985). SEQUENCE FROM N.A. MEDLINE-S60120978; Pubmed=3511471; SEQUENCE FROM N.A. MEDLINE-S60120978; Pubmed=3511471; "Evolution and organization of the human protein C gene."; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; "Evolution and organization of the human protein C gene."; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. SUBMITTED (JUN-2001) to the EMBL/GenBank/DDBJ databases. SQUENCE OF 106-461 FROM N.A. MEDLINE-84272714; Pubmed=6589623; FOSTER D.C., Davie E.W.; "Characterization of a cDM coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [5] MILETICH J.P., Broze G.J. Jr.; MEDLINE-90293994; Pubmed=1694179; Miletich J.P., Broze G.J. Jr.; MEDLINE-90293994; Pubmed=1694179; Miletich J.P., Broze G.J. Jr.; "Embalation may influence the frequency of usage at asparagine-X-cysteine sites."; J. Biol. Chem. 265:11397-11404(1990).	≨	
precursor and its messenger RNA, based upon the DNA sequence of cloned human liver CDNAs"; Nucleic Acids Res. 13:533-5247(1985). Nucleic Acids Res. 13:533-5247(1985). SEQUENCE ROW N.A. MEDILINE-66120978; PubMed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SUBMILTEd (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] Scoton D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [6] SEQUENCE OF 106-461 FROM N.A. MEDLINE-84272714; PubMed-6589623; SCOTON NATL. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] YEAR CONTINEAGE SITE ASN-371. MEDLINE-90293094; PubMed-1694119; Miletich J.P., Broze G.J. Jr.; MEDLINE-90293094; PubMed-1694119; Miletich J.P., Broze G.J. Jr.; Beta protein C is not 91ycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites.; J. Biol. Chem. 265:11397-11404(1990).	r.	acid human
cloned human liver cDNAs."; Nucleic Acids Res. 13:5233-5247(1985). [3] SEQUENCE FROW N.8. MEDLINE-86120978; Pubmed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; FVOILUTION and organization of the human protein C gene."; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Rieder M.J. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [6] SEQUENCE OF 106-461 FROW N.A. MEDLINE-84272714; Pubmed-6589623; FOSTER D.C., Davie B.W.; FOSTER D.C., Davie B.W.; Froc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). GARBOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; Submitted at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites.; J. Biol. Chem. 265:11397-11404(1990).	r.	the DNA sequence
Nucleic Acids Res. 13:5233-5247(1985). Nucleic Acids Res. 13:5233-5247(1985). SEQUENCE FROM N.A. MEDLINE=66120978; Pubmed=3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Plutzky J., Hoskins J.A., Edge G.L., Poel C.L., Y1 Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Nickerson D.A.; Submitted (JUN-201) to the EMBL/GenBank/DDBJ databases. [5] SUBJUNCE OF 106-461 FROM N.A. MEDLINE-64272714; Pubmed-6589623; FOSTER D.C., Davie E.W.; CARROHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; "Beta procretin C is not glycosylated at asparagine-X-cysteine sites."; J. Biol. Chem. 265:11397-11404(1990).	닯	cloned human liver cDNAs.";
[5] [6] EQUENCE FROM N.A. MEDILINE-66120978; PubMed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] Submitted G. M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM. N.A. MEDLINE-84272714; PubMed-6589623; SCOSTED LC., David E.W.; ROSTED LC., David E.W.; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] CARBOHYDRATE-INKAGE SITE ASN-371. MEDLINE-90293094; PubMed-1694179; Miletich J.P., Broze G.J. Jr.; Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites.; J. Biol. Chem. 265:11397-11404(1990).	7	
SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-86120978; PubMed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Froc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [6] Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [6] Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [6] Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [7] Characterization of a conA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). CARBOHYDRATE-INKAGE STTE ASN-371. MEDLINE-90293094; PubMed-1694179; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Submitted Steel asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X- Cysteine sites. J. Biol. Chem. 265:11397-11404(1990).	Z.	[3]
MEDLINE-86120978; Pubmed-3511471; Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; "Evolution and organization of the human protein C gene."; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). Sci. Sci. Sci. U.S.A. 83:546-550(1986). Subnitted (JUN-201) to the EMBL/GenBank/DDBJ databases. Sci. UNA-201) to the EMBL/GenBank/DDBJ databases. Sci. Sci. Sci. Sci. Sci. U.S.A. 81:4766-4770(1984). Sci. U.S.A. 81:4766-4770(1984). Sci. U.S.A. 81:4766-4770(1984). Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; "Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites."; J. Biol. Chem. 265:11397-11404(1990).	КP	SEQUENCE FROM N.A.
Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; "Evolution and organization of the human protein C gene."; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Ridder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. MEDLINE-84272714; Pubmed-6589623; SEQUENCE OF 1.C., Davis E.W.; "Characterization of a cDNA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] SEQUENCE OF 106-461 FROM coll of a cDNA coding for human protein C."; ROSSED D.C., Davis E.W.; "Characterization of a CDNA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] Miletich J.P., Broze G.J. Jr.; "Miletich J.P., Broze G.J. Jr.; "Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites."; J. Biol. Chem. 265:11397-11404(1990).	ž	MEDLINE-86120978; PubMed-3511471;
"Evolution and organization of the human protein C gene."; Proc. Natl. Acad. Scl. U.S.A. 83:546-550(1986). SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 NICKERSON D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROW N.A. MEDLINE-84272714; PubMed-6589623; FOSTER D.C., Davie E.W.; FOSTER D.C., Davie E.W.; FOSTER D.C., Davie E.W.; FOSTER D.C., Davie E.W.; MICHARCHIAGE STIE ASN-371. MEDLINE-80293094; PubMed-1694179; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; SEGUENCE OF 106-401800 A Sparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-Cysteine sites." J. Biol. Chem. 265:11397-11404(1990).	Ş	Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;
Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986). [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Yl Nickerson D.A.; Submitted (JUN-201) to the EMBL/GenBank/DDBJ databases. [5] SUBDITE 401 FROM N.A. SEQUENCE OF 106-461 FROM N.A. SEQUENCE OF 106-461 FROM N.A. SEQUENCE OF 106-401 FROM N.A. "Characterization of a cDNA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] SEAROHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; "Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X- Cysteine sites."; J. Biol. Chem. 265:11397-11404(1990).	RI	"Evolution and organization of the human protein C gene.":
SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE OF 106-461 FROM N.A. MEDLINE-84272714; Pubmed-6589623; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). CARBOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Sebta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-Cysteine sites.; J. Biol. Chem. 265:11397-11404(1990).	R.	Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).
SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Y1 Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] REDITURE-04.27.2714; PubMed-6589623; FOSTER D.C., Davie E.W.; FOSTER D.C., Davie E.W.; FOSTER D.C., Davie E.W.; FORAROHYDRATE-LINKAGE SITE ASN-371. MILETCH J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; FEARDHYDRALE C.B. Not 91.00971ated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-Cysteine sites. J. Biol. Chem. 265:11397-11404(1990).	Z	[7]
Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Yi Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. MEDDINE-8472714; Pubmed-6589623; FOSTER D.C., Davie E.W.; acDNA coding for human protein C.*; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). [6] MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Sebta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-Cysteine sites.*; J. Biol. Chem. 265:11397-11404(1990).	0	W NOGG GUNGHOGH
Nickerson D.A., Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE OF 106-461 FROW N.A. MEDLINE-84272714; Pubmed-6589623; Foster D.C., Davie E.W.; Foster D.C., Davie E.W.; Foster D.C. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984). GABOHYDRATE-LINKAGE SITE ASN-371. MEDLINE-90293094; Pubmed-1694179; Miletich J.P., Broze G.J. Jr.; Miletich J.P., Broze G.J. Jr.; Belta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites.; J. Biol. Chem. 265:11397-11404(1990).	. 6	÷
	5 5	1
	≨ ;	NICKELSON DIAN.
	2	Submitteed (JON-2001) to the Embildent/UDBS databases.
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	КР	SEQUENCE OF 106-461 FROM N.A.
	ž	MEDLINE-84272714; Pubmed-6589623;
	æ	Foster D.C., Davie E.W.;
	F	q for human protein
	된	4766-4770(1984).
	N.	9
	RP	CARBOHYDRATE-LINKAGE SITE ASN-371.
	×	WEDI INE-90293094 - Dibbed-1694179 -
	4	Miletich I D. Broze G. J. Tr.
	Ę	"Reta protein C is not allocaviated at asparagine 329, the rate of
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J. Biol.		ctationary may introduce our including or could be deprivated and other states of course of the states of the stat
[7]		T Taiol Chem 265.11397-11404/1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91329836; PubMed-1868249; Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.; "The spectrum of genetic defects in a panel of 40 Dutch families with symptomatic protein C deficiency type I: heterogeneity and founder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugahara Y., Miura O., Yuen P., Aoki N.;
"Proctein C deficiency Hong Kong 1 and 2: hereditary protein C
deficiency caused by two mutant alleles, a 5-nucleotide deletion and
a missense mutation.";
                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
MEDLINE-97157472; PubMed-9003757;
Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmon C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Hereditary thrombophilia: identification of nonsense and missense mutations in the protein C gene.";
Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
                                                                                                                                                                        MEDLINE-94272342; PubMed-8003977;
Fisher C.L., Greengard J.S., Griffin J.H.;
Models of the serine protease domain of the human antithrombotic
plasma factor activated protein C and its zymogen.";
Protein Sci. 3:588-599(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cooper D.N.;
"Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in the protein C gene causing thrombosis.";
Nucleic Acids Res. 17:10513-10513(1989).
                                             Harris R.J., Ling V.T., Spellman M.W.; "O-linked fucose is present in the first epidermal growth factor domain of factor XII but not protein C."; J. Biol. Chem. 267:5102-5107(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REDITION ON PROC VARIANTS.
MEDILINE-93190290; PubMed-8446940;
Reliama P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
Sala N., Cooper D.N.;
"Protein C deficiency: a database of mutations. For the Protein
Subcommittee of the Scientific and Standardization Committee of
International Society on Thrombosis and Haemostasis.";
Thromb. Haemost. 69:77-84(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87204221; PubMed-2437584;
Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90098906; PubMed-2602169;
Grundy C.B., Chitolie A., Talbot S., Bevan D., Kakkar V.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Protein CVermont: symptomatic type II protein C deficiency associated with two GLA domain mutations."; Blood 79:1456-1465(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS ALA-62 (VERMONT-1) AND MET-76.
MEDLINE-92190481; PUDMed-1347706;
BOY111 E.G., Tomczak JA., Grant B., Bhushan F., Pillemer
Rainville I.R., Long G.L.;
  HYDROXYLATION.
MEDLINE-92184750; PubMed-1544894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARÍANT ASP-418 (HONG KONG-2).
MEDLINE-92305321; PubMed-1611081;
                                                                                                                                                          3D-STRUCTURE MODELING OF 175-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT LEU-289.
MEDLINE-92380660; Pubmed-1511988;
                                                                                                                                                                                                                                                                                                                                                                                                  "The 2.8 A crystal structu
EMBO J. 15:6822-6831(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT TRP-211 (LONDON-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                effects.";
Blood 78:890-894(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         slood 80:126-133(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT CYS-444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT CYS-272.
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VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
MEDLINE-9412329; Pubmed=8292730;
Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
Koerper M.A., Coughlin J., Griffin J.H.;
"Genefic mutations in ten urrelated American patients with
symptomatic type 1 protein C deficiency ";
Blood Coagul. Fibrinolysis 4:791-796(1993);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto K., Matsushita T., Sugiura I., Takamatsu J., Iwasaki E., Wada H., Deguchi K., Shirakawa S., Saito H.; "Homozygous protein C deficiency: identification of a novel missense mutation that causes impaired secretion of the mutant protein C."; J. Lab. Clin. Med. 119:682-689(1992).
                                                                                                                                                                                               VARIANTS GLN-220 AND TRP-220.
MEDLINE-92380661; PubMed=1511989;
Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
"Two different missense mutations at Arg 178 of the protein C (PROC)
gene causing recurrent venous thrombosis.";
Hum. Genet. 89:685-686(1992).
Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
"A novel homozygous missense mutation in the protein C (PROC) gene
causing recurrent venous thrombosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A GLA domain mutation (Arg 15-->Trp) in the protein C (PROC) gene causing type 2 protein C deficiency and recurrent venous
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WEDLINE-94001606; PubMed-8398832;
Marchetti G., Patracchini P., Gemmati D., Castaman G., Rodeghiero I Wacchti G., Patracchini P., Gemmati D., Bernardi F.;
"Symptomatic type II protein C deficiency caused by a missense mutation (Gly 381-->Ser) in the substrate-binding pocket.";
Br. J. Haematol. 84:285-289(1993).
SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gandrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M., Gouault-Heilman M., Toulon P., Fiessinger J.N., Goossens M.; "Two novel mutations responsible for hereditary type I protein C deficiency: characterization by denaturing gradient gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Twelve novel and two recurrent mutations in 14 Austrian families with hereditary protein C deficiency."; Blood Coagul. Fibrinolysis 4:273-280(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
MEDILES-93313192; PubMed-8324221;
Gandrille S., Alhen-Gelas M., Gaussem P., Aillaud M.-F., Dupuy
Juhan-Vague I., Alach M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H., Bertina R.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blood Coagul. Fibrinolysis 4:345-347(1993).
                                                                                       thrombosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT GLN-220.
MEDLINE-93250852; PubMed-1301959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92276939; PubMed=1593215;
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                                                                                                                    Genet. 89:683-684(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hum. Mutat. 1:491-500(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blood 82:159-168(1993).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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TISSUE SPECIFICITY: PLASKA; SYNTHESIZED IN THE LIVER.

PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.

MISCELLANEOUS. CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO SITE IS NECESSARY FOR THE RECOGNITION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide structure and characterization of the murine gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994)
-1- FUNCTION: PROTEIN C. IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                      PRTC_MOUSE STANDARD; PRT; 461 AA.
P33687; 035498;
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitaninr & dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-129/SvJ;
MEDLINE-9815576; PubMed-9493582;
Jalbert L.R., Rosen E.D., Lissens A., Carmellet P., Collen D.,
Castellino F.J.;
                                                                                                                                                                                                                                                                                                                                 MEDLINE-92316897; PubMed-1618739;
Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
"Isolation and characterization of a mouse protein C cDNA.";
J. Blochem. 111:491-495(1992).
           Length 461;
                               11; Indels
                                                        44
                                                                            86
                                                                   43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH
                                                        1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THROMBIN-THROMBOMODULIN COMPLEX. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
        Score 160; DB 1;
Pred. No. 9.1e-20;
2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticoagulant protein C.";
Thromb. Haemost. 79:310-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94318474; PubMed-8043441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 274-434 FROM N.A.
        81.2%;
70.5%;
                                31; Conservative
                     Similarity
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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          Query Match
                     Local
                     Best Loca
Matches
                                                                                                                              PRTC_MOUSE
                                                                                                                   RESULT 2
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noved. Usage by and for commercial (See http://www.lsb-slb.ch/announce/
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Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endotherlal cell; Hydrolase; Signal.
1 33 BY SIMILARITY.
PROPEP 34 41 BY SIMILARITY.
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PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
EGF-LIKE 1.
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modified and this statement is not removed. Usage by and for con
entities requires a license agreement (See http://www.isb-sib.ch/au
or send an email to license@isb-sib.ch).
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HYDROXYLATION (BY SIMILARITY)
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GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
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SMART; SM00019; EGE_L1ke; I.
SMART; SM00001; EGE_L1ke; I.
SMART; SM00020; GLA; I.
FROSITE; PS00100; ASX_HYDROXYL; I.
FROSITE; PS01180; EGE_L; I.
FROSITE; PS01180; EGE_L; I.
FROSITE; PS01180; EGE_CA; I.
FROSITE; PS00111; GLU_CARBOXYLATION; I.
FROSITE; PS00114; FRYPSIN_LDON; I.
FROSITE; PS00134; TRYPSIN_LIS; I.
FROSITE; PS00134; TRYPSIN_LIS; I.
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Interpro; IPR001383; GLA_blood.
Interpro; IPR001254; Ser_protease_fry.
Interpro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                           InterPro; IPR000152; Ask_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-11ke.
                                                                                EMBL; D10445; BA01235.1; -. EMBL; AF034569; AAC33795.1; -.
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                                                                                                                                EMBL; D43755; BAA07812.1;
PIR; JX0210; JX0210.
HSSP; P04070; 1PCU.
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Gamma-carboxyglutamic acid; Calcium-binding, Vitamin K; Hydroxylation,
EGF-like domain, Repeat; Endothelial cell; Hydrolase; Signal.
SIGNAL
BY SIMILARITY.
PROPEP 33 41 BY SIMILARITY.
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PROFEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
EGF-LIKE 1.
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PIR; S24312; S24312.
HSSP; P04070; 1PCU.
MEROPS; S01.218; -.
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      C -1 SUBUNIT: SYRTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENGRME IS THEN ACTIVATED BY THROMEN WHICH CLEAVES A TETAADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMODOTED BY THROMEOMODILIN.

C -1 - TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

C -1 - PTM: THE VITAMIN K-DEPENDENT, ENZYMENTIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROFIED TO SIND CALCIUM.

MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMEOMODULIN COMPLEX.

C -1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

C -1 - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institution as in there are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Vitamin-K dependent protein C precursor (BC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
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                                                                                                                                                                                                                                          Score 140; DB 1;
Pred. No. 2.6e-16;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            461 AA
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TISSUE-Liver;
MEDLINE-92329550; PubMed-1627650;
                                                                                                                                                                                                                51945 MW;
                                                                                                                                                                                                                                            71.1%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                          26; Conservative
                                                                                           254
387
426
214
                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
    104
1121
1139
1146
1161
1182
238
3398
3398
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                                                                                                                         DISULFID
                                                                                                                                                                   CARBOHYD
CONFLICT
CONFLICT
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                                                               DISULFID
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                                                                                             DISULFID
                                                                                                                                                                                                              SEQUENCE
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                                                 DISULFID
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    PHILLIE HELLES
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Query Match
Best Local Similarity
Matches 26; Conserv
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CARBOHYD
SEQUENCE
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                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOCETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS A FEACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.

-1 TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-1- PTM: THE VITAMIN N -DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLD RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
-1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE. BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprochrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                        Length 461;
        INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                           Indels
                                                                                  BA4CF93664EDACD5 CRC64;
                                                                                                                                                1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                           42 ANSFLEEVRAGSLERECMEEICDFEEAQEIFQNVEDTLAFWIKY
                                                                                                                 3.9e-16;
                                                                                                       DB 1;
                                                                                                                59.1%; Pred. No. 3.9e
tive 7; Mismatches
                                                                                                                                                                                                                         458 AA
  SIMILARITY
                                                                                                        Score 139;
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InterPro; IPR000561; EGF-like.
                                                                                   X.
                                                                                                       70.68;
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                                                                                                                           26; Conservative
                                                                                                                                                                                                                        STANDARD;
                                                                                 461 AA;
                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE-Liver;
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Q28661;
                                                            CARBOHYD
CARBOHYD
SEQUENCE
                                        DISULFID
DISULFID
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Best Local 5
                    DISULFID
                               DISULFID
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STATITIES
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Blood coagulation; Glycoprotein; Serine protease; Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation; EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.

NON_TER 1 1 1 1 1 1 1 SIMILARITY.
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(BY SIMILARITY).
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CLEAVAGE (BY THROMBIN) (BY SIMILARITY)
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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BY SIMILARITY.

BY SIMILARITY.

VITAMIN K-DEPENDENT PROTEIN C.

PROTEIN C LIGHT CHAIN (BY SIMI PROTEIN C HEAVY CHAIN (BY SIMI
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HYDROXYLATION (BY SIMILARITY).
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BY SIMILARITY.
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BY SIMILARITY.
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GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC
(BY SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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Pred. No. 5.7e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-LIKE 2.
SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
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BY SIMILARITY
                                                                                 Pfam: PF00594; 91a: 1.

SMART: SM00181; EGF: 2.

SMART: SM00069; GLA: 1.

SMART: SM000009; GLA: 1.

PROSITE: PS00010; ASX_HYDROXYL: 1.

PROSITE: PS01082; EGF_1: 1.

PROSITE: PS01187; EGF_2: 2.

PROSITE: PS01187; EGF_CA: 1.

PROSITE: PS00011; GLU_CARBOXYLATION: 1.

PROSITE: PS00011; GLU_CARBOXYLATION: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-LIKE 1
              InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
                                                                                                                                                                                                                                                                PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51087 MW;
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ilarity 59.1%;
Conservative
EGF_Ca.
                                                Pfam; PF00008; EGF; 2.
Pfam; PF00008; trypsin; 1.
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458
458
458
458
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250
296
399
58
58
105
114
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                                                                                                                                                                                                                                                                                                                                                                                                                            GUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a retardecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

TISSUE SPECIFICITY: Plasma; synthesized in the liver.

PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the
                                                                                                                                                                                                                                                                                                                                            Kim H.K.W.;
"Porcine factor V: cDNA cloning, gene mapping, three-dimensional
protein modeling of membrane binding sites and comparative anatomy of
                                                                                                                                                                                                                                                                                                  Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
                                                                                                                         16-OCT-2001 (Rel. 40, Last account)
15-OCT-2001 (Rel. 40, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                      1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombin-thrombomodulin complex. SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                            459 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002383; GGP_Ca.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Ser_protease_Iry.
InterPro; IPR000294; VitK_dep_GLA.
'fam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                   MEDLINE-21121490; PubMed-11229814;
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EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000152; Asx_hydroxyl
InterPro; IPR001314; Chymotrypsin
                                                                                                                  16-OCT-2001 (Rel. 40, Created)
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gla; 1.
                                                                                           STANDARD;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                    Sus scrofa (Pig).
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                                                                                                                                                                          actor XIV).
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BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                                                                                                                                                                                                                                (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
HYDROXYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                      SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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                                                                                                                                                                                        PROTEIN C HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                  GAMMA-CARBOXYGLUTAMIC
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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Pred. No. 2.2e-13;
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       SMART; SM00181; EGF; 2.
SMART; SM00001; EGF_11ke; 2.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL;
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.38;
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GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.4
Best Local Similarity 52.3
Matches 23; Conservative
                                                                                                                                                                                       459
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175
459
47
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PRINTS; PR00001;
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SEQUENCE
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and VIIIa.
SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENTYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.
TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-85014826; Pubmed-6091100;
Long G.L., Balagaje R.M., McG1111vray R.T.A.;
"Cloning and sequencing of liver cDNA coding for bowine protein C.";
Proc. Natl. Acad. Sci. U.S.A. 81:5553-5556(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-83213513; PubMed-6304092; Esmon N.L., Debault L.E., Esmon C.T.; Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless protein C.";
                                                                                       PRTC_BOVIN

ID PRTC_BOVIN

ID PRTC_BOVIN

ID CON145;

DT 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 13-AUG-1987 (Rel. 41, Last annotation update)

DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)

DE (Autoprothrombin IA) (Anticoagulant protein C) (Blood coagulation DE factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 40-194.
MEDLINE-83007325; Pubmed-6896876;
Fernlund P., Stenflo J.;
*Amino acid sequence of the light chain of bovine protein C.";
J. Biol. Chem. 257:12170-12179(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
"Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83007326; PubMed-6896877; Stenflo J., Fernlund P., Stenflo Stenflond P., Farnlund P., J. Anno acid sequence of the heavy chain of bovine protein C."; J. Biol. Chem. 257:12180-12190(1982).
               42 ANSFLEELRPSSLERECKEETCDFEEAREIFQNTENTMAFWSKY
1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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                                                                                                                                                                                                                                                                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 197-456.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
MISCELLANDEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
SITE IS NECESSARY FOR THE RECOGNITION OF THE
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PROTEIN C HEAVY CHAIN.
ACTIVATION PEPTIDE.
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GAMMA-CARBOXYGLUTAMIC
GAMMA-CARBOXYGLUTAMIC
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GAMMA-CARBOXYGLUTAMIC
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                            THROMBIN-THROMBOMODULIN COMPLEX.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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TRYPSIN_HIS; FALSE_NEG.
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Pfam; PF00089; EGF; 2.
Ffam; PF00089; Lrypain; 1.
Ffam; PF00089; Lrypain; 1.
SWART; SW00181; EGF; 2.
SWART; SW00069; GLA; 1.
SWART; SW000069; GLA; 1.
SWART; SW000069; GLA; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01180; EGF_2; 2.
PROSITE; PS01187; EGF_2; 2.
PROSITE; PS0101187; EGF_2; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; PROSITE; PS00011; GLU_CARBOXYLATION; PROSITE; PS000136; TRYPSIN_JES; PALSE, PROSITE; PS00136; TRYPSIN_JES; PALSE, PROSITE; PS00136; TRYPSIN_JES; PALSE, PROSITE; PS00136; TRYPSIN_SER; 1.
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InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF_Ca.
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Biochem. 218:153-163(1993)
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"Localization of the str
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                     ACTIVE
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Inoue K., Morita T.;
Indentification of O-linked oligosaccharide chains in the activation
peptides of blood coagulation factor X. The role of the carbohydrate
moleties in the activation of factor X.";
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        Fung M.R., Campbell R.M., McGillivray R.T.A.;
"Blood coagulation factor X mRNA encodes a single polypeptide chain
containing a prepro leader sequence.";
Nucleic Acids Res. 12:4481-4492(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Amino acid sequence of the light chain of bovine factor X1 (Stuart
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
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13.-MG-1987 (Rel. 05, Last sequence update)
15.-UNN-2002 (Rel. 41, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McMullen B.A., Fujikawa K., Kisiel W.; "The occurrence of beta-hydroxyaspartic acid in the vitamin
                                                                                                                                Length 456;
                                                                                                                                                   12; Indels
                                                                                                   -> PV (IN REF. 4).
CAAF6833F894C209 CRC64;
                                               N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
F -> K.
VP -> PV (IN REF. 4).
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                                                                                                                                                                       1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWS 42
                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975),
                                                                                                                              Score 122; DB 1;
Pred. No. 3.3e-13;
); Mismatches 12
                                                                                       -> K.

-> PV (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-dependent blood coagulation zymogens.";
Blochem. Blophys. Res. Commun. 115:8-14(1983).
                                                                                                                                                                                                                                          492 AA
  SIMILARITY.
 BY SIMILARI
INTERCHAIN.
                                                                                                                                                                                                                                         PRT;
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                                                                                                              51407 MW;
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SEQUENCE OF 1-487 FROM N.A.
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289
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366
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159
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455 AA;
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15-JUN-2002
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SEQUENCE OF
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MEDLINE-91084483; PubMed-2261466; Selander M., Persson E., Stenflo J., Drakenberg T.; HINMR assignment and secondary structure of the Ca2(+)-free form of the amino-terminal epidermal growth factor like domain in coagulation
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"Activation of bovinne factor X (Stuart factor): conversion of factor
Xa-aipha to factor Xa-bera.";
Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
                                                       Neurath H., Davie E.W.; "Bovine factor). Evidence of homology
                             litani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
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Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
Calcium-binding properties of bovine factor X lacking the gamma-
carboxyglutamic acid-containing region.";
J. Biol. Chem. 259:5705-5710(1984).
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MEDLINE-96387194; PubMed-8794734;
Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Localization of the structural difference between bovine blood coagulation factors X1 and X2 to tyrosine 18 in the activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92406922; PubMed-1527084; Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O., Stenflo J., Drakenberg T.;
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MEDLINE-92329412; PubMed-1627540;
Ullner M., Selander M., Persson E., Stenflo J., Drakenberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide.";
J. Biol. Chem. 261:4008-4014(1986).
                                                                                                                         with mammalian serine proteases.";
Blochemistry 11:4899-4903(1972).
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MEDLINE=73053314; PubMed=4264286;
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RESULT 8
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                                         PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY). OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY). MINCELLANBOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATION.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
MAX BE REMOVED BUT IS NOT NECESSARY FOR
           OF SOME
BIND
MORE DISULFIDE BONDS.
PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
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                                   PTM: N- AND O-GLYCOSYLATED
                                                                                                                                                                      EMBL; X00673; CAA25286.1; --
PIR; A00925; EXBO.
PDB; IAPO; 31-JAN-94.
PDB; ICCF; 31-MAY-94.
PDB; IWHE; 15-MAY-97.
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SEQUENCE FROM N.A.
MEDIINE-91216473; PubMed-1902434;
Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
"Cloning and expression in.COS-1 cells of a full-length cDNA encoding human coagulation factor X.";
Gene 99:291-294(1991).
                                                                                                                                  Gaps
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MEDLINE-8325207; PubMed-6871167;

MEDLINE-8325207; PubMed-6871167;

Kwa E.Y., Weinstein B.;

"Complete amino acid sequence of the light chain of human blood coagulation factor X: evidence for identification of residue 63 as beta-hydroxyaspartic acid.";

Bjochemistry 22:2875-2884(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
MEDLINE-86221713; PubMed-3011603;
Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
"Isolation and characterization of human blood-coagulation factor
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leytus S.P., Foster D.C., Kurachi K., Davie E.W.; "Gene for human factor X: a blood coagulation factor whose gene organization is essentially identical with that of factor IX and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 13-488 FROM N.A.
MEDLINE-85216545; PubMed-2582420;
MEDLINE-85216545; C.W., McGillivray R.T.A.;
McGillivray R.T.A.;
"Characterization in almost full-length cDNA coding for human blood coagulation factor X.";
Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
                                                                                                                                  ö
                                                                                                                                                                                                                                                                                          P00742; Q14340;
21-07L-1986 (Rel. 01, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor X precursor (EC 3.4.21:6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.; "Characterization of a cDNA coding for human factor X.";
                                                                                                Length 492;
                                                                                                                                Indels
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
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                                                                                                                                                                  44
                                                                                                                                                                                 1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                              Score 114; DB 1; L
Pred. No. 8.6e-12;
8; Mismatches 16;
                                                                                                                                                                                                                                                                              488 AA
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MEDLINE-84222026; PubMed-6587384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blochemistry 25:5098-5102(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 19-488 FROM N.A.
                                                                                                               45.5%;
                                                                                                57.9%;
                                                                                                               Best_Local Similarity 45.5
Matches 20; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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PROSITE; PS00020; Tryp_SFC; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS010186; EGF_2; 1.
PROSITE; PS01187; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation; Gamma-carboxyglutcanic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; EGF_like domain; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 488;
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GAMMA - CARBOXYGLUTAMIC ACID.
GAWMA - CARBOXYGLUTAMIC ACID.
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O-LINKED (GALNAC. .).
N-LINKED (GLCNAC. .).
FIId—CAR_000012.
N-LINKED (GLCNAC. .).
/FIId—CAR_000013.
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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                                                                                                                               InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001861; EGF_1.
InterPro; IPR001881; EGF_2.
InterPro; IPR001881; EGF_C.
InterPro; IPR001283; GIA_blood.
InterPro; IPR001284; Ser_protease_Try.
Pfam; PF000089; EGF; 2.
Pfam; PF00009; EGF; 2.
Pfam; PF00089; Trypsin; 1.
Pfam; PF00594; gla; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00701; GIABLOOD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                  SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM00069; GLA; 1.
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                                                                      GlycoSuiteDB; P00742;
Genew; HGNC:3528; F10.
MIM; 134530; -.
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              PDB; 1KKA; 23-MAR-99.
PDB; 1KKA; 23-MAR-99.
PDB; 1KKB; 23-MAR-99.
                                                           MEROPS; S01.216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- PTM: N- AND O-GLYCOSYLATED.
-1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                          SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
MEDILINE-94062825; PubMed-8243461;
Inoue K., Morita T.;
"Identification of O-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate moleties in the activation of factor X. The role of the carbohydrate Eur. J. Biochem. 218:153-163(1993).
                                                                                                                                               MEDLINE-90128299; PubMed-2612918;
Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhushanam K., Lyman G.;
"Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.";
Gene 84:517-519(1989).
                                                                                                                                                                                                                                                                                                                                                                                         Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
"Structural basis for chemical inhibition of human blood coagulation
factor Xa.";
                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
MEDLINE-93360277; PubMed=8355279;
Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W. Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
"Structure of human des(1-45) factor Xa at 2.2-A resolution.";
J. Mol. Biol. 232:947-966(1993).
                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
MEDLINE-98283982; PubMed-9618463;
Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
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AAA52486.1;
AAA52636.1;
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A24478; A24478.
1HCG; 08-MAY-95.
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EMBL; EMBL; EMBL;

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                                                                                                                                                                                                                    MEDLINE-9726311: PubMed-9101642;
Pendurth! U.R., Anderson K.D., James H.L.;
Thromb. Res. 85:503-514(1997).
-1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholiplid during blood clotting.
-1- CATALYIIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then Arg-1-Ibe bonds in prothrombin to form thrombin.
-1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINCIE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
                                                                                                          (Rabbit), hortebrata; Euteleostoml; nordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
-1- SIMILARITY: CONTAINS 2 EGP-LIRE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SC
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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InterPro; IPR000294; Vitk_dep_GLA.
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PS00010; ASX_HYDROXYL; 1.
PS00022; EGF_1; 1.
PS01186; EGF_2; 2.
PS01181; EGF_CA; 1.
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EGF-like.
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Interpro; IPR002383; GLA_blood
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SMART; SM00001; EGF_11ke; 1.
SMART; SM00069; GLA; 1.
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                                                                                                                Oryctolagus cuniculus
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                   15-DEC-1998 (15-DEC-1998 (15-JUN-2002 (
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                       Gaps
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                     ö
                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.3%; Score 107; DB 1; Length 231; 43.9%; Pred. No. 5.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN 3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8A373E4848490D81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid; Vitamin K; Transmembrane.
                                                        44
                                                                             20 ANEFLEELRQGTIERECMEEICSYEEVKEVFENKEKTMEFW 60
                                                        1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
 Pred. No. 4.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 490 AA.
                                                                                                                                                                                       231 AA.
                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00740; ICFH.
InterPro; IPR002383; GLA_blood.
InterPro; IPR002383; GLA_blood.
InterPro; IPR00294; Vitk_dep_GLA.
Pfam; PF00594; gla; 1.
PRIMTS; PR00001; GLABLOOD.
SMART; SM00069; GLABLOOD.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF326350; AAK00955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25848 MW;
43.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gamma-carboxyglutamic
                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 AA;
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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FA10_RABIT
ID FA10_RABIT
                                                                                                                                                                                   TMG3_HUMAN
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TRANSMEM
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DOMAIN
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CHAIN

Best Loca Matches

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Phromb. Res. Suppl. 69:231-238(1993).
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GLU_CARBOXYLATION;
TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWART; SM00179; EGF_CA; 1.
SWART; SW00001; EGF_like; 1.
SWART; SM00069; GLA; 1.
PROSTIE: PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolass.
           (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00722; CHYMOTRYPSIN, PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U7747; AAB37326.1; -. HSSP; P08709; 1FAK.
           Oryctolagus cuniculus
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                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50240;
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                                     NCBI_TaxID-9986;
                                                                                                                              REVISION TO 395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00011
                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00594;
                                                                                                    factor VII.";
                                                                IISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; 1
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Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
                                                                       EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL). EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FA7_RABIT STANDARD; PRT; 444 AA.
98139; P79224;
01-FEB-1996 (Rel. 33, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
3A39FAB5AF2AGDII CRC64;
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                                                               ACTIVATED FACTOR XA, HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                    HYDROXYLATION (BY SIMILARITY).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                                         GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
                                                                                                   SAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                                                                                                        (BY
                                                                                                                                                                   SIMILAKITY).
GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                                                                                                                                                                           SIMILARIII).
GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                                                                   GAMMA-CARBOXYGLUTAMIC ACID (BY
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                                                                                                                                                                                                                                            SIMILAKIII).
GAMMA-CARBOXYGLUTAMIC ACID (BY
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                                                                                                                                                                                                                                                                                    GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                                                                                                                                                                                                                                                SIMILAKITI).
GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.3%; Score 103; DB 1; Length 490; 43.2%; Pred. No. 6.8e-10; 1ve 9; Mismatches 16; Indels
                                                                                                                                                                                                            GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                        SAMMA-CARBOXYGLUTAMIC
                         BY SIMILARITY.
FACTOR X LIGHT CHAIN.
FACTOR X HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 ANSFLEELKKGNLERECMEENCSYEEALEVFEDREKTNEFWNKY
                                                      ACTIVATION PEPTIDE
                                                                                         SERINE PROTEASE.
         EGF-like domain; Repeat.
20 POTENTIAL.
                                                                                                                                                                  SIMILARITY)
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61
187
205
490 AA;
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hes 19; Conserv
         lgnal; Zymogen;
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DISULFID
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CARBOHYD
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                   SIGNAL
                           PROPEP
                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
Ruiz S.R., Blajchman M.A., Clarke B.J.;
Submitted (NOV-1996) to the EMBL/Genbank/DDBJ databases.
Submitted (NOV-1996) to the EMBL/Genbank/DDBJ databases.
-1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR XIA.
THOWNERIED TO FACTOR VIIA BY FACTOR XA, FACTOR XIA.
THROMBIN BY MINOR PROFECLYSIS. IN THE PRESENCE OF TISSUE FACTOR
AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
BY LIMITED PROFECULYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
SIMILARITY).
                                                                                                                                                                                                                                                                      MEDLINE-93190306; PubMed-8383365;
Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
"Complete nucleotide sequence of the cDNA encoding rabbit coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease; Blood coagulation; Zymogen; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-11e bond in factor X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     form factor Xa.
SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULETIDE BOND (BY SIMILARITY).
TISSUE SPECIFICITY: PLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: THE VITAMIN K-DEPENDENT, BNZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eu
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALCIUM (BY SIMILARITY), SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR001742; EGF_2.
InterPro; IPR001881; EGF_C.
InterPro; IPR001881; GIA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GIA.
Pfam; PF00008; EGF; 2.
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seqid1_mod.rsp

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Davie E.W.;
                                                                                                                                                                                                                                                                                                                                                                          ö
Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.

1 21 POTENTIAL.
                                                                                                       CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
FACTOR IXA, OR THROMBIN) (BY SIMILARITY).
BY SIMILARITY.
                                                                        EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                      HYDROXYLATION (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-66205965; Pubmed-3486420; Grant F.J.; Saari G.C., Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J.; Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kisiel W., Kurachi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 444;
                                                                                                                                                                            BY SIMILARITY.
CARBOXYCGUTAMIC ACID.
GAMMA-CARBOXYCGUTAMIC ACID.
GAMMA-CARBOXYCGUTAMIC ACID.
GAMMA-CARBOXYGUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Indels
                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (PO 0481ABC4FE5427F8 CRC64;
                                         FACTOR VII LIGHT CHAIN FACTOR VII HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 1;
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 ANSFLEELRPGSLERECKEELCSFEEAREVFOSTERTKQFW
                                                                                              SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                               GLA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                              49011 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                               (Rel. 06, (Rel. 06, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                               444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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P08709; Q14339;
01-JAN-1988 (RE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606
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SEQUENCE
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                                                                                                                            ACT_SITE
                                                                                                                                                                                                    DISULFID
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MOD_RES
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                                        CHAIN
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SITE
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                                ROPEP
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STRUCTURE OF CARBOHYDRATE ON SER-112.
MEDLINE-91344709; PubMed-2129367;
Iwanaga S., Nishimura H., Rawabbita S., Kistel W., Hase S., Ikenaka T.;
"A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";
Adv. Exp. Med. Biol. 281:121-131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE OF CARBOHYDRATE ON SER-112.
MEDIATE-90062160; Pubmed-2511201;
Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
Silmonishi Y., Iwanaga S.,
"Identification of a disaccharide (Xyl-Glc) and a trisaccharide
(Xyl2-Glc) O-glycosidically linked to a serine residue in the first
epidermal growth factor-like domain of human factors VII and IX and
protein Z and bovine protein Z.";
J. Blol. Chem. 264:20320-20325(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89088153; Pubmed-3264725;
Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
Pedersen A.H., Hedner U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells."; slochemistry 27:7785-7793(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang E., St Charles R., Tulinsky A.; Structure of extracellular tissue factor complexed with factor VIIa
                                                                                                                              SEQUENCE FROM N.A.

MEDLINES 2560948 P.D., Dubwed-3037537;
O'Hara P.G., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
Hagen F.S., Murray M.J.;
Hagen F.S., Murray M.J.;
Nuclectide sequence of the gene coding for human factor VII, a
vitamin K-dependent protein participating in blood coagulation.*;
Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF MEDLINE-96175641; Pubmed-8598903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91250411; PubMed-1904059; Blocar S., Foster D.C., Thim L., Wherg F.C., Christensen M., Komlyama-Y., Pedersen A.B., Kisiel W.; Human plasma and recombinant factor VII. Characterization of Oglycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine."; Blol. Chem. 266:11051-11057(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drakenberg T.; "Solution structure of the N-terminal EGF-like domain from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445. Refeder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., X1 Q., Nickerson D.A.; Toth E.J., Submitted (JAN-2002) to the EMBL/Genbank/PDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
Characterization of a cDNA coding for human factor VII.";
roc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 105-145.
MEDLINE-98367502; PubMed-9692950;
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Biochemistry 37:10605-10615(1998),
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                                                                                                                                                           Marchetti G., Patracchini P., Gemmati D., Derosa V., Pinotti M., Rodorigo G., Casonato A., Girolani A., Bernardi F.; "Detection of two missense mutations and characterization of a repeat Polymorphism in the factor VII gene (F7)."; Hum. Genet. 89:497-502(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94264305; PubMed-8204879; Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W., Roberts H.R., Blajchman M., Monroe D.M., High K.A.; "Severe factor VII deficiency caused by mutations abolishing the Cleavage site for activation and altering binding to tissue factor."; Blood 83:3524-3535(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bernardi F., Castaman G., Redaelii R., Pinotti M., Lunghi B.,
Rodeghiero F., Marchetti G.;
"Topologically equivalent mutations causing dysfunctional coagulation
factors VII (294Ala-->Val) and X (334Ser-->Pro).";
Hum. Mol. Genet. 3:1175-1177(1994).
                                                                 "Purification and characterization of factor VII 304-Gln: a variant molecule with reduced activity isolated from a clinically unaffected
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Lunghi B., Rodeghiero F., Marchetti G.;
"Mutation pattern in clinically asymptomatic coagulation factor VII
deficiency.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arbini A.A., Mannucci P.M., Bauer K.A.;
A ThriSyMet mutation in factor VII of a patient with a hereditary
deficiency causes defective secretion of the molecule.";
Blood 87:5085-5094(1996).
                                                                                                                                                                                                                                                                                                                                                                                        Tuddenham E.G.D., McVey J.H.;
"Detection of missense mutations by single-strand conformational polymorphism (SSCP) analysis in five dysfunctional variants of coagulation factor VII.";
                                    Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J., eade T.W., Tuddenham E.G.D.;
                                                                                                                                                                                                                                                        MEDLINE-93372811; PubMed-8364544;
Marchetti G., Ferrati M., Patracchini P., Redaelli R., Bernardi A. miscesses mutation (178cys-->Tyr) and two neutral dimorphisms (115His and 333Ser) in the human coagulation factor VII gene."; Hum. Mol. Genet. 2:1055-1056(1993).
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94061028; PubMed-8242057;
Takamiya O., Kemball-Cook G., Marin D.M.A., Cooper D.N.,
von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95064662; PubMed-7974346;
Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Factor VII Mie: homozygous asymptomatic type I deficiency an amino acid substitution of His (CAC) for Arg(247) (CGC)
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MEDLINE=97001216; Pubmed=8844208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalytic domain.";
Thromb. Haemost. 71:773-777(1994).
                                                                                                                                                   MEDLINE-92340074; PubMed-1634227;
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MEDLINE-95072589; PubMed-7981691;
                         MEDLINE-91300046; PubMed-2070047;
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                                                                                                                                    VARIANTS GLN-364 AND PHE-370
                                                                                                          3lood 78:132-140(1991).
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                                                     Meade T.W.
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Hum. Mutat. Suppl. 1:S189-S191(1998).

-!- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Prolinerich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A., Felice A.E.;
in the coagulation
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PHARMACEUTICAL: Available under the names Niastase or Novose (Novo Nordisk). Used for the treatment of bleeding episodes
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                                                                                                                                                                                Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir
Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
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PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO
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Pred. No. 3.1e-09;
4; Mismatches 17;
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Alshinawi C., Scerri C., Galdies R., Aquilina
"Two new missense mutations (P134T and A244V)
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                  Zaizov R., Seligsohn U.;
"Ala244Val is a common, probably ancient mu
deficiency in Moroccan and Iranian Jews.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS MALTA THR-194 AND VAL-304.
                                                                                                                                                                                                                                                                                                                                                                                                                           Thromb. Haemost. 76:283-291(1996).
                                                                                                                                         PubMed-8883260;
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Mutat. 8:108-115(1996).
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Best Local Similarity
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                                                                                        VARIANT VAL-304.
MEDLINE=97037613;
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014668;
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"Partial characterization of vertebrate prothrombin cDNAs:

"Partial characterization of vertebrate prothrombin cDNAs:

"partial characterization of vertebrate prothrombin from nine different species.";

Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

-I-FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND. IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

-I-CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-Gly; activates fibringen to fibrin and releases fibrinopeptide A and B.

-I-FTH: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Indels
                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26538A61AB0AEB98 CRC64;
                                                                                                                                                                                              InterPro: IPR002383; GLA_blood.
InterPro: IPR000294; VitK_dep_GLA.
Priam. PR000594; 91 1.
PRINTS; PR00001; GLABLOOD.
SMART; SM00069; GLA; 1.
PROSITE; PS00001; GLU_CARBOXYLATION; 1.
Gamma-carboxyglutamic_acid; Vitamin K; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92; DB 1; I
Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                 PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUB-Liver; MEDLINE-90332426; PubMed-2377469; Dihanich M., Monard D., "CDMA sequence of rat prothrombin."; Nucleic Acids Res. 18:4251-4251(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                   GLA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92212913; PubMed-1557383;
                                                                                                                                EMBL; AF009242; AAB67070.1; -. HSSP; P00740; 1CFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24947 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 383-617 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                  HGNC:9469; PRRG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  131 1
218 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
                                                                                                                                                                                    MIM; 604428;
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
DOMAIN
DOMAIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THRB_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                 PROPEP
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            ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
OF PROTHROWBIN TO THROWBIN.
MISCELLANGOUS: PROTHROWBIN IS ACTIVATED ON THE SURFACE OF A
PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
VITSELE HAS TO BE ACTIVATED BY THE INITIAL, SWALL AMOUNTS OF
 RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
                                                                                                                                                                                             -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRACMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY PACTOR XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO0134; TRYPSIN_HIS; I. PROSITE; PSO0134; TRYPSIN_HIS; I. PROSITE; PSO0135; TRYPSIN_SER; I. Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; Hydrolase; Serine protease; Kringle; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THROMBIN LIGHT CHAIN (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERINE PROTEASE.
CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA)
CLEAVAGE (BY FACTOR XA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM (SYSTEM (SYSTEM (
                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SCHARGE RELAY SCHARGE RELAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1505; PROTHROMBIN.
PRODOM; PD000195; Kringle; 2.
SMART; SM00169; GLA; 1.
SMART; SM00130; RK; 2.
SMART; SM00130; RK; 2.
SMART; SM0011; GLA; 1.
PROSITE; PS00011; GLU_CARBOXILATION; 1.
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS50240; RRINGLE_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMORY) SULLALY, MEMORY MEMORY INTERPROJUENT CHARACTER PROMOTORY KATHOLE. PRINTS; PROMOTORY CLARACTER MEMORY PROMOTORY CHARACTER PRINTS; PROMOTORY KATHOLE. PRINTS; PROMOTORY KATHOLE. PRINTS; PROMOTORY KATHOLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52835; CAA37017.1; -. EMBL; M81397; AAA42240.1; -. PIR; S10511; S10511. HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.217;
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ACT_SITE
ACT_SITE
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DOMAIN
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DOMAIN
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            RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDES BY A MICROSOMAL ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDES CHARGED PHOSPHOLIPLO SUFFACE WHICH IS ESSENTIAL FOR THE CONVERSION OF PROTHROWEN TO THROMBIN IS ARE CENTROWED TO THROMBIN IS ACCURANCED IN THE CAPTROMBIN IS ACCURANCED IN THE SENDING BY SUFFACE OF A PHOSPHOLIPLD MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR VITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                           MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRACMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
   PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS0001; Tryp_SPC; 1.
PROSITE; PS0001; GLU_CARBOXILATION; 1.
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS50070; KRINGLE_2; 2.
PROSITE; PS500134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PHOG coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; SIGNAL 1.

24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION PEPTIDE (FRAGMENT
ACTIVATION PEPTIDE (FRAGMENT
THROMBIN LIGHT (A)
THROMBIN HEAVY CHAIN (A)
                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTHROMBIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000001; Kringle.
Interpro; IPR003966; Prothrombin.
Interpro; IPR001254; Ser_protease_Try.
Interpro; IPR000294; VitK_dep_GLA.
Pfam; PF000051; Kringle; 2.
Pfam; PF000059; trypsln; 1.
Pfam; PF00099; trypsln; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.217; -.
MEROPS; S01.217; -.
MED; MGI B8380; F2.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52308; CAA36548.1; -.
EMBL; M81394; AAA40435.1; -.
PIR; A35827; A35827.
HSSP; P00734; 1B7X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRODO18; KRINGLE.
PRINTS; PRO1505; PROTHROMBIN.
ProDom; PD000395; Kringle; 2.
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SMART; SM00130; KR; 2.
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325
361
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   <u>+</u>
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Banfield D.K., Macgillivray R.T.; "Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thrombin from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Gly; activates fibrinogen to fibrin and releases fibrinopeptide A and B.
           GAMMA-CARBOXYGUDTAMIC ACID.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6; TISSUE-Liver;
MEDLINES-91025551; PubMed=2222810;
Ericaner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
Fitzgibbon J.J., Pal, J.A., Chapman V.M., Elliott R.W.;
"Characterization of the cDNA coding for mouse prothrombin and
localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                        43.9%; Score 86.5; DB 1; Length 617; 42.2%; Pred. No. 6.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                              AD27D1B71445DB1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANS-FLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDIDVFWAKY 88
 GAMMA-CARBOXYGLUTAMIC
GAMMA-CARBOXYGLUTAMIC
GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.2e; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              70411 MW;
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617 AA;
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nes 19; Conserv
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rissue-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THRB_MOUSE
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CARBOHYD
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Matches
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                              Length 618;
                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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42.2%; Pred. No. 6.2e-07;
tive 6; Mismatches 19; Indels
                                                                                                    GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                        B89F719AAFD601E0 CRC64;
                                                                                                                                                                                                                                                                                                             553 N
70268 MW;
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Best Local Similarity 42.28
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                  413
553
618 AA;
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DISULFID
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1 ANS-FLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44 44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWARY 88 ò g

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Gaps

Search completed: May 15, 2003, 13:27:34 Job time: 13 secs

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May 15, 2003, 13:24:56 ; Search time 28 Seconds (without alignments) 323.788 Million cell updates/sec
                                                                                                                                                                                        SEGID1_MOD
197
1 ANSFLXXLRQGSLXRXCIXX.....XXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                          671580
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rodent:* sp_plant:*

sp_bacteriap:*

sp_archeap:* ap_rvirus:*

sp_invertebrate:*

Database

sp_organelle:*

sp_mammal:* sp_mhc:*

	Description	O9ttrO canis famil	Q91wn8 mus musculu	Q99pc6 mus musculu	063207 rattus norv	O54740 mus musculu	Q99132 mus musculu	O88947 mus musculu	Q96pq8 homo sapien	Ogamag ornithorhyn	Q9nsd0 homo sapien	Q16519 homo sapien	Q15253 homo sapien	Q8t613 halocynthia	Q61109 mus musculu	Q14316 homo sapten	Q95nd7 pan troglod
SUMMARIES	QΙ	Q9TTRO	1 Q91WN8	1 Q99PC6	1 Q63207	1 054740	1 099132	1 088947	Q96PQ8	O9GMD9	09NSD0	016519	Q15253	Q8T613	1 Q61109	014316	Q95ND7
	Query Match Length DB	456 6	460 1	460 1	482 1	481 1	481 1	.481 1	701 4	469 6	650 4	650 4	100	542 5	446 1	456 4	461 6
ø	Query	9.94	71.1	68.0	58.4	51.3	51.3	51.3	50.3	48.2	43.1	43.1	42.6	41.9	40.6	40.6	40.6
	Score	151	140	134	115	101	101	101	66	95	82	82	84	82.5	80	80	80
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095nd6 pan troglod 028994 sus scrofa 091001 gallus gall 029094 sus scrofa 090ykl brachydanlo	Ogewa mus musculu Ogewa mus musculu P82607 notechis sc Ogetwa struthio ca Ogewa musculu Ogesis homo sapien Ogeris mus musculu Ogesis musculu Ogesis mus musculu Ogesis sativ Ogesis asativ Ogesis arabidopsis Ogesis oryza sativ
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461 6 138 6 607 13 648 6 433 13	50 99 99 99 99 99 99 99 99 99 99 99 99 99
40.6 39.6 39.6 37.6	22222222222222222222222222222222222222
80 78 78 73.5	88 88 88 88 88 88 88 88 88 88 88 88 88
17 18 19 20 21	

RESU 09TT	QOTTRO OSTITO DESTINATING DE	44
a S	Q9TTRO FRELLMINAKI;	
55	01-MAY-2000 (TrEMBLrel. 13,	ed)
i E	01-MAR-2002 (TrEMBLrel. 20, Last	Last annotation update)
DE S	Protein C precursor.	
SO	_	
ဗ	Eukaryota; Metazoa;	
႘	Mammalla; Eutheria;	Carnivora; Fissipedia; Canidae; Canis.
ŏ	NCBL_TaxID=9615;	
R P	SEQUENCE FROM N.A.	
RA		M., Matis U., Brunnberg L.,
RA		
RT		promosomal assignment of the canine
RI		•
RL		
RN		
RP		
RX		
Æ		ope A., Brenig B.;
RT		polymorphisms.";
RL		
ပ္ပ		ASE FAMILY S1; ALSO KNOWN AS THE
ပ္ပ	TRYPSIN FAMILY.	
DR		
DR	NSSP; P04070; 1PCU.	
DR	MEROPS; S01.218;	
DR	InterPro;	
DR	InterPro; IPR001314;	
DR	InterPro; IPR000561;	
DR	InterPro;	
D,R	InterPro; IPR002383;	
DR	InterPro; IPR001254;	_Try.
DR	InterPro; IPR000294;	
DR	R Pfam; PF00008; EGF; 2.	

ALIGNMENTS

δ a

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Gaps
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                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00135; TRXPSIN_SEK; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
11; Indels
                                                                 42 ANSFLEEMRPGSLERECMEEICDFEEAQEIFONVEDTLAFWIKY 85
                                            1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Anticoagulant protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

68.0%; Score 134; DB 11;
Best Local Similarity 56.8%; Pred. No. 1.4e-14;
Matches 25; Conservative 7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10n; Repeat; Serine protease.
460 AA; 51784 MW; 0293BC25E9D3ED16
                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 AA
7; Mismatches
                                                                                                                                                                                                     460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0022; EGF_1; UNKNOWN_1.
PROSITE; PSO1186; EGF_2; 2.
PROSITE; PSO01197; EGF_CA: 1.
PROSITE; PSO0011; GLU_CARBOXYLATION; 1.
PROSITE; PSO0134; TRYPSIN_LOM; 1.
PROSITE; PSO0134; TRYPSIN_LIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001881; EGF_Ca.
InterPro; IPR001283; GLA_blood.
InterPro; IPR001284; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00181; EGF; 2.
SMART; SM00001; EGF_like; 2.
SMART; SM00069; GLA; 1.
SMART; SM000069; Tryp_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000152; Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete sequence of UC72A01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00722; CHYMOTRYPSIN, PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYBEIN FAMILY.
EMBL; AF318182; AAK07918.1;
HSSP: P04070; 1PCU.
26; Conservative
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:97771; Proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydroxylation;
SEQUENCE 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                   Q99PC6
Q99PC6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q63207
Q63207;
Matches
                                                                                                                                                       RESULT 3
Q99PC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              063207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                            R SMART; SM00181; EGF; 2.

SMART; SM00069; GLA; 1.

SMART; SM00000; Tryp_SPC; 1.

R PROSITE; PS00010; ASX_HYDROXYL; 1.

R PROSITE; PS01186; EGF_2; 2.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS010117; EGF_CA; 2.

R PROSITE; PS010117; EGF_CA; 1.

R PROSITE; PS010114; TRYPSIN_LDOM; 1.

R PROSITE; PS010134; TRYPSIN_LDOM; 1.

R PROSITE; PS001034; TRYPSIN_LSER; 1.

R PROSITE; PS001034; TRYPSIN_LSER; 1.

R PROSITE; PS001034; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
PROTEIN C LIGHT CHAIN.
PROTEIN C CONNECTING DIPEPTIDE.
PROTEIN C HEAVY CHAIN.
7AD3A8C1C34E59FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.6%; Score 151; DB 6; Length 456; 63.6%; Pred. No. 1.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013896; AAH13896.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease.
; 51818 MW; 0117F26E68FCC274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 140; DB 11;
Pred. No. 1.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF_CA; UNKNOWN_1.
GLU_CARBOXYLATION; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00089; trypsin; 1, PR0SITE; PS00010, ASX_HPNBXXL; UNKNOWN_1 PROSITE; PS00012; EGF 1; UNKNOWN 1. PROSITE; PS01186; EGF_2; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
           PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50813 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.18;
59.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similar to protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Labes 28; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291WN8;
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Heidtmann H.H., Kontermann R.E.; "Cloning and recombinant expression of mouse coagulation factor X."; Thromb. Res. 92:33-41(1998).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWART; SM00179; EGF_CA: 1.

SWART; SM00001; EGF_Ike; 1.

SWART; SM00001; EGF_Ike; 1.

SWART; SM000020; Tryp_SPC: 1.

PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01186; EGF_1: UNKNOWN_1.

PROSITE; PS01186; EGF_2: 2.

PROSITE; PS0011; GLU_CARBOXYLATION; 1.

PROSITE; PS0011; GLU_CARBOXYLATION; 1.

PROSITE; PS00134; TRYPSIN_LIS: UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_LIS: UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_LIS: UNKNOWN_1.

Calcium_binding; EGF_1ke domain; Glycoprotein; Hydrolage; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.3%; Score 101; DB 11; Length 481; Best Local Similarity 38.6%; Pred. No. 7.4e-09; Matches 17; Conservative 10; Mismatches 17; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 481 COAGULATION FACTOR X.
481 AA; 53986 MW; CF702DE5EF9D97AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANSFLXXLRQGSLXRXCIXXICDFXXARXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 ANSFEBERKGNLERECMEBICSYEEVREIFEDDEKTKEYWTKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 AA
                                                                                                                                                                                                                                                                                                                 MEDINGES, 201.110;
MEDINGES, 201.110;
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001283; GIA_blood.
InterPro; IPR001284; SGI_Protease_Try.
InterPro; IPR001294; VitK_dep_GIA.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; Irrypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN,
PRINTS; PR00012; CHYMOTRYPSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                         MEDLINE-98454993; Pubmed-9783672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease; Signal
                                                                                                                                                                                                                                                    EMBL; AJ222677; CAA10933.1;
HSSP; P00742; 1XKA.
MEROPS; S01.216; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21, Coagulation factor X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                        SEQUENCE FROM N.A.
       NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  099L32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     099L32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
Q99L32
            SOTETER WALL BOOK A STREET OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-96093186; Pub.Hed-8578539;
Stanton C., Ross R.P., Whitson S., Wallin R.;
Evidence for competition between vitamin K-dependent clotting factors for intracellular processing by the vitamin K-dependent gamma-
                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pBluescript.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                          carboxylase.";
Thromb. Res. 80:63-73(1995).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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R INTERPROJ 1PR0001314; Chymotrypain.

R INTERPRO; IPR0001314; Chymotrypain.

R INTERPRO; IPR0001314; Chymotrypain.

R INTERPRO; IPR000561; EGF_2.

R INTERPRO; IPR000124; EGF_2.

R INTERPRO; IPR001254; SGR_DIOOd.

R INTERPRO; IPR001254; SGR_DIOOd.

R Pfam; PF00008; EGF; 2.

R Pfam; PF00008; EGF; 2.

R Pfam; PF00008; EGF; 2.

R PRINTS; PR001729; CHYMOTRYPSIN.

R PRINTS; PR00001; GLABLOOD.

SMART; SM000001; GGF_LIKe; 1.

SMART; SM000000; EGF_LIKe; 1.

R SMART; SM000000; EGF_LIKe; 1.

R SMART; SM00010; EGF_LIKe; 1.

R PROSITE; PS00010; ASK_HYDROXYL; 1.

R PROSITE; PS01186; EGF_C3; 1.

R PROSITE; PS01186; EGF_C3; 1.

R PROSITE; PS01187; EGF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        054740 PRELIMINARY; PRT; 481 AA. 054740; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Coagulation factor X precursor (EC 3.4.21.6).
  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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43.2%; Pred. No. 2.8e-11;
:lve 10; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydroxylation; Repeat; Serine protease.
SEQUENCE 482 AA; 54265 MW; 0284678E3954A698
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X79807; CAA56202.1; -. HSSP; P00742; 1XKA.
01-NOV-1996 (TrEMBLrel, 01, 01-NOV-1996 (TrEMBLrel, 01, 01-MAR-2002 (TrEMBLrel, 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 43.29
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                                                                                                                                                                              NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F10 OR FA10.
                                                                             Factor X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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Gaps

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"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.3%; Score 101; DB 11; Length 481; 38.6%; Pred. No. 7.4e-09; Live 10; Mismatches 17; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 COAGULATION FACTOR X.
54018 MW; 8AC09DE5EF9D271E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Factor VII active site mutant immunoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-21477448; Pubmed-11593034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                   MGD; MGI:103107; F10.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF272774; AAX58886.1; ...
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                   R000561; EGF-11ke
                        EMBL; AF211347; AAF22980.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca
InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu Z., Garen A.;
                                                                                                                                                                   InterPro; IE
                                                                                      MEROPS; S01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98347933; PubMed=9684791;
Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
Castellino F.J., Rosen E.D.;
"Cloning and characterization of a cDNA encoding murine coagulation
factor X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00011; GIU_CARBOXYLATION; 1.
PROSITE; PS00101; TRYPSIN_DOM; 1.
PROSITE; PS001034; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS001035; TRYPSIN_SER; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooper A., Liang Z., Castellino F.J., Rosen B.D.;
Clouning and Characterization of the Murine Factor X Gene.";
Thromb. Haemost. 0:0-0(2000).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.3%; Score 101; DB 11; Length 481; 38.6%; Pred. No. 7.4e-09; Live 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||| ::|:| | |: || : ||| 41 ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Coagulation factor X precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
                                   MEROPS; SO1.216;
MCD: MCI:101107; F10.
MCD: MCI:101107; F10.
MCD: MCI:101107; F10.
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001341; EGF_21.
InterPro: IPR001431; EGF_C3.
InterPro: IPR001431; EGF_II.
InterPro: IPR0013434; EGF_II.
InterPro: IPR0012343; GIA_blood.
InterPro: IPR001234; Ser_protease_Iry.
InterPro: IPR001234; Ser_protease_Iry.
InterPro: IPR001234; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_1; UNKNOWN_1.
EGF_2; 2.
EGF_CA; 1.
GLU_CARBOXYLATION; 1.
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STRAIN-C57BL6 X CBA; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 38.6%; Pre-Matches 17; Conservative 10;
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                                                                                                                                                                                                                                                                                                    Pfam: PF00089; Trypsin; 1.
PRINES; PR0072; CHYMOTRYPSIN.
PRINES; PR00010; EGFBLODD.
PRINTS; PR00001; GLABLOOD.
EMBL; BC003877; AAH03877.1;
HSSP; P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00181; EGF; 2.
SMART; SM00001; EGF_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                          Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00022
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PROSITE; PS01187
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SEQUENCE 481
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RESULT 7 088947

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PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Repeat;
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A., Dahlback B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 650;
                                                                                                              Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; X12892; CAA31383.1; -.
HSSP; P00740; 1CFH.
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Indels
                             PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 469 AA; 52196 WW; 4C66C230D0758F6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 POTENTIAL.
72480 MW; C67345ECE8645174 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ANSLLEETKQGNLERECIEELCNKEEAREVFENDPETDYFYPRY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Protein S precursor.
                                                                                                                                                                                 1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWS 42
                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 43.1%; Score 85; DB 4; 1
Best Local Similarity 38.6%; Pred. No. 6.1e-06;
Matches 17; Conservative 10; Mismatches 17,
                                                                                                                48.2%; Score 95; DB 6;
40.5%; Pred. No. 7.9e-08;
                                                                                                                                              7; Mismatches
                                                                                                                                                                                                                                                                                                   650 AA.
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PROSITE; PS50240; TRYPSIN_DOM; 1.
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016519;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00001; GLABLOOD.
SWART; SM00179; EGF_CA; 3.
SWART; SM00069; GLA; 1.
SRART; SM00282; LamG; 2.
PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001881; EGF_Ca.
InterPro; IPR00283; GLA_blood.
InterPro; IPR001791; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR000152; Asx_hydroxyl nterPro; IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00594; gla; 1.
Pfam; PF00054; laminin_G; 1.
                                                                                                           Query Match
Best Local Similarity 40.5%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSUE-LIVER;
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SIGNAL
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                                                                                                                                                                                                                                                                RESULT 10
Q9NSD0
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Q16519 .
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MEDILINE-21015017; PubMed-11132153;
MEDILINE-21015017; PubMed-11132153;
POORAfShar M., Aveskoph M., Munday B., Hellman L.;
"Identification and structural analysis of four serine proteases in importeme, the platypus, Ornithorhynchus anatinus.";
"Immunogenetics 52:19-28(2000).
"Immunogenetics 52:19-28(2000).
"YAYPSIN FAMILY.

EMBL: AR275654; AAG00453.1; -.
HSSP; P00742; 1XKB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ornithorhynchus anatinus (Duckbill platypus).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
NCBI_TaxID-9258;
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                   Length 701;
                                                                                                                                                                                                                                                                                               / Match 50.3%; Score 99; DB 4; Length 701
Local Similarity 48.8%; Pred. No. 2.5e-08;
hes 20; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                  77826 MW; 94AC6CEB42CC992F CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ornith-Line factor X.
                                                                                                                                                                                                                                                                                                                                                                                                61 ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFW 101
                                                                                                                                                                                                                                                                                                                                                                  1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                        PFGMM: PF00089; trypain; 1.
SMART; SM00181; EGF; 2.
PROSITE; PS00010: ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS001010: ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS001186; EGF_2; UNKNOWN_1.
PROSITE; PS00119; EGF_CARBOXYLATION; UNKNOWN_1.
PROSITE; PS00209; IG_MHC; UNKNOWN_1.
PROSITE; PS00214; TRYPSIN_DOM; 1.
PROSITE; PS00114; TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01187; EGF_CA; 1.
PS00011; GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00022; EGF_1; UNKNOWN_3
PS01186; EGF_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                  Hydrolase; Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                  701 AA;
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                                               am; PF00047;
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PROSITE;
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                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                               Matches
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InterPro; IPR002383; GLA_blood.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00594; gla; 1.
PRINTS; PR000001; GLABLOOD.
SWART; SW00069; GLA; 1.
PROSITE; PS00011; GLU_CARBOXILATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                             36.48;
                                                                                                                                                                         Query.Match.
Best Local Similarity 36.4
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                      43
>100
100
                                                                                                                                                  100 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gla-like protein
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                                                                                                                                    NON TER
SEQUENCE
                                                                                        Signal.
SIGNAL
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                                                                                                                      CHAIN
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PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS000102; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
Calcium-binding; EGF_like domain; Glycoprotein; Hydroxylation; Repeat;
                                                                                                                                               MEDLINE-86313649; PubMed-2944113;
Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.
                                                                                                                                                                                    "Isolation and age of the cDNA for human protein S, a regulator of blood coagulation.";
Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
EMBL. MA338; AAA60181.1;
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MacGillivray R.T., Irwin D.M., Guinto E.R., Stone J.C.;
"Recombinant genetic approaches to functional mapping of thrombin.";
Ann. N. Y. Acad. Sci. 485:73-79(1986).
HSSP; P00735; 2PF1.
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.1%; Score 85; DB 4; Length 650
38.6%; Pred. No. 6.1e-06;
tive 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN S.
9A8C044C503BF474 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                 InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR001791; Laminin_G.
InterPro; IPR000294; VitK_dep_GLA.
                              Protein S precursor (Fragment).
                                                                                                                                                                                                                                                                                              IPR001881; EGF_Ca.
IPR002383; GLA_blood.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72462 MW;
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00594; 9la; 1.
Pfam; PF00594; 9la; 1.
PRINTS; PR00001; GLABLOOD.
SMART; SM00179; EGE_CA; 3.
SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                        Fam; PF00008; EGF; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650
                                                         Homo sapiens (Human).
                                                                                                                                                                               Stenflo J., Wydro R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 AA;
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                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                 InterPro;
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SECUENCE FROM N.A.

Wang C.-P., Stafford D.W.;

Wang C.-P., Stafford D.W.;

"Halocynthia roretzi gla-like protein partial genomic DNA sequence.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF466701; AAL74247.2;

EMBL; AF466701; AAL74247.2;

SEQUENCE 542 AA; 62090 MW; EB9BF13FE42B32FE CRC64;
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Castellino F.J.;
"Characterization of a cDNA encoding murine coagulation factor VII.";
Thromb. Haemost. 75:481-487(1996).
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                 Length 100;
                                                                                                                                                                      . 1.2e-06;
tches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                       11302 MW; FD0E5D0174E1F6FE CRC64;
                                                                                                                                                                                                                                                                                                  1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 SHFEELQQGNLERECYEELCSFEEAREVFETNIQDLNEFWAKY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8T613;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SFLXXLRQGSLXRXCIXXICDFXXAKXIFE-DVDDTLAFWSKH 44
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Last annotation update)
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41.9%; Score 82.5; DB 5;
Best Local Similarity 34.9%; Pred. No. 1.3e-05;
Matches 15; Conservative 10; Mismatches 17;
                                                                                                                                              Score 84; DB 4;
Pred. No. 1.2e-06
8; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 AA.
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POTENTIAL.
                              POTENTIAL.
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Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat; Serine protease. SEQUENCE 456 AA: 51140 MM. ELLONGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 QGNLERECMEEKCSFEEAREVFENTERTTEFWKQY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 QGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00010, ASX_HYDROXYL; UNKNOWN_1.
PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; 2.
PS01187; EGF_CA; 1.
PS00011; GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50340; TRYPSIN_DOM: 1.
PS00134; TRYPSIN_HIS; UNKNOWN_1.
PS00135; TRYPSIN_SER: 1.
                                                                                     Interpro; IPR000561; EGF-11kē.
Interpro; IPR000742; EGF_2.
Interpro; IPR001438; EGF_Ca.
Interpro; IPR001438; EGF_II.
Interpro; IPR001383; GLA_blood.
Interpro; IPR001254; Ser_protease_Try.
Interpro; IPR000294; VltK_dep_GLA.
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                                               Asx_hydroxyl
                                                                                                                                                                                                                                                                                              Pfam: PF00089; trypsin; 1,
PRINTS, PR0072; CHYMOTRYPSIN.
PRINTS; PR00010; BGFBLOOD.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                               Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas disease, HAEMOPHILIA B)) (Factor IX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The putalive factor IX gene promoter in hemophilia B Leyden.";
11.00d 72:1074-1076(1988).
1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 11; Length 446;
Pred. No. 2.9e-05;
3; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird C.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASX_HYDROXYL; UNKNOWN_1.
CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00020; Tryp_SPc; 1.
PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
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GLU_CARBOXYLATION; 1.
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Interpro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
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                                                                                                                                         Chymotrypsin.
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MEDLINE-88327116; Pubmed-3416069;
                                                                                                                                                            ; Crystallin.
; EGF-like.
                                                                                                                                                                                                                              GLA_blood
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PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.6%;
ilarity 43.9%;
Conservative
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EMBL; X55008; CAB38245.2; -.
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; EGF_11ke; 1

    GLABLOOD.

EMBL; U44795; AAC52570.1;
HSSP; P08709; 1FAK.
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Best Local Similarity
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SEQUENCE 446
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May 15,

2003, 13:26:41; Search time 15 Seconds

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Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.

Searched:

262574 seqs,

29422922 residues

Title: Perfect score:

SEQID1_MOD 197

ANSFLXXLRQGSLXRXCIXX.....XXAKXIFEDVDDTLAFWSKH

Sequence:

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                              GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
LENGTH: 44
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                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: MOD_RES ; LOCATION: (0)...(0) ; COCATION: (0)...(0) ; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic US-08-955-636-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-955-636-24
                                                                                                                                                                                US-08-955-636-35
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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08955636A
Patent NO. 6017882
GEMERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYDEPTIDES
FILE REFERENCE: 09531/002001
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/955,636A CURRENT FILING DATE: 1997-10-23 NUMBER OF SEQ ID NOS: 35 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 24 LENGTH: 44 TYPE: PRT
                                                                                                                                                          Sequence 35 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
                     TYPE: PRT
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                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                          35, Application US/08955636A
5. 6017882
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US-09-658-5-536-23
US-08-955-636-2
US-08-374-042-2
US-08-484-558-2
US-08-487-037-3
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US-08-487-037-3
US-08-487-037-1
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US-08-955-471-3

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Description

Patent No.

5270178-17 5270178-18 5460953-3

US-08-229-280-5 US-09-065-872-2 5270178-2

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US-08-756-506-2 US-08-756-506-4 5270178-13

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Database

Issued_Patents_AA:*

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2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

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US-08-955-636-20
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                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 20, Application US/08955636A Patent No. 6017882
                    Query Match
Best Local
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APPLICANT: Nelsestu
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                                                                                                                                                                                                                                                                                                                                APPLICANT: Nelsestuen, Gary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT ITLE OF INVENTION: POLYPEPTIDES LE REFERENCE: 09531/002001
                                                                            FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
                                                                                                                                              LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
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LOCATION: (0)...(
                Local Similarity
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97.7%;
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97.7%;
                86.3%;
95.5%;
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                Score 170; DB 3; Pred. No. 4e-22;
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US-08-955-636-1

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Sequence 1, Application US/08955636A Patent No. 6017882

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, NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic US-08-955-636-22
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US-08-955-636-19
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                                                                                                                                                                                                                         SEQ ID NO 22
LENGTH: 44
TYPE: PRT
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Best Local :
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                                                                Matches
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                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT TITLE OF INVENTION: POLYPEPTIDES FILE REFERENCE: 09531/002001
                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/955,636A CURRENT FILING DATE: 1997-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPFIDES
FILE REFERENCE: 09531/002001
                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nelsestuen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: 18-955-626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD_RES
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                                                              Local Similarity es 42; Conserv
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ANSFLXXLRDSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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42; Conserv
                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 3.0
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                                                                Conservative
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                                                                             95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.5%;
                                                                           Score 168; DB 3;
Pred. No. 8.9e-22;
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Pred. No. 8.9e-22;
0; Mismatches 2
                                                                                            Length 44;
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GENERAL INFORMATION:

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; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-1
                                                                                                                                                                               RESULT 9
US-08-965-832-2
                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic
US-08-955-636-25
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Best Local Similarity 90...
40; Conservative
                                                                                                                                          sequence 2, Application US/08965832
Patent No. 5847085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 44
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
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TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
FILE REFERENCE: 09531/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Nelsestuen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/955,6361
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
EQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/955,636A CURRENT FILING DATE: 1997-10-23 NUMBER OF SEQ ID NOS: 35
                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Nelsestuen,
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tent No. 601788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 44
                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                       APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV
                  STREET:
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                        1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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                                     ADDRESSEE:
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Peachtree Street
                 2800 One Atlantic Center, 1201 West
                                                                                                                                                                                                                                                                                                                               Conservative
                                  Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                              81.2%;
93.2%;
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90.9%;
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Pred. No. 2e-20;
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RESULT 10
US-08-295-411-1
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                                                                                                                                                                                                                                                                      Sequence 1, Application Patent No. 5679639
GENERAL INFORMATION:
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                    APPLICANT: Mesters, FITITLE OF INVENTION: STITLE OF INVENTION: A
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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APPLICATION NUMBER: 08/
FILING DATE: 8-NOV-1996
                                                                                                                                                   NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                           APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
OTHER INFORMATION: /note- "where Xaa means
OTHER INFORMATION: carboxylglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OM
                                                                                                  ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute STREET: 10666 No. 5679639th Torrey Pines Road, TPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 7-NOV-1997
                                   COUNTRY: UZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                   La Jolla
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                     Serine Protease-Derived Polypeptides Anti-Peptide Antibodies, Systems and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 160; DB 2;
Pred. No. 2.1e-20;
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Therapeutic Methods
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US-08-955-471-1
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                    Patent No. 596875
                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                          APPLICANT:
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LOCATION: 158..169
OTHER INFORMATION:
OTHER INFORMATION:
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nes 31; Conserv
COMPUTER: IBM PC
OPERATING SYSTEM:
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OTHER INFORMATION:
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                            MEDIUM TYPE:
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                                                                      COUNTRY: USA
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                                                             92037
                                                                                                 SSEE: Research Institute
T: 10666 No. 5968751th Torrey Pines Road, TPC
La Jolla
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170..419
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                            Floppy disk
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PC-DOS/MS-DOS
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                                                                                                                                                                                                                                           Rolf M.
                                                                                                                                                                                               for Inhibiting Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Protein C Activation
Peptide"
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                                                 GRGANISM: Homo sapiens US-09-667-570A-3
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LOCATION: 170..419
OTHER INFORMATION:
US-08-955-471-1
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                                                                                                                  SEQ ID NO 3
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Patent No. 6436397
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Best Local Similarity
Query Match
Best Local Similarity
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                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/045,255
PRIOR FILING DATE: 1997-04-28
                                                                                                                                                                                                                                  APPLICANT: Sheliga, Theodore A TITLE OF INVENTION: Improved Methods for Processing Activated Protein FILE REFERENCE: X-11796A
                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                APPLICANT: Baker,
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                                                                                   TYPE: PRT
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                                                                                               LENGTH: 419
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APPLICATION NUMBER:
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LOCATION: 158..169
OTHER INFORMATION:
OTHER INFORMATION:
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Carlson, Andrew D
Huang, Lihua
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Peptide"
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 Score 160; DB 4; Pred. No. 2.7e-19;
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                                            Matches
                                                                     Query Match
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                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11Hem.
MOLECULE TYPE: pro
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LOCATION: 158..169
OTHER INFORMATION: OTHER INFORMATION: I
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CITY: La
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                                                                                                                           NAME/KEY:
LOCATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                OTHER INFORMATION:
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                                                        Local
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1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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10666 North Torrey Pines Road, TPC 8
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                                           Conservative
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170..419
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                                                                                                               /note= "Protein C Heavy Chain"
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Peptide"
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US-08-756-506-4
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Best Local Similarity
Matches 31; Conserv
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                                      APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
                CORRESPONDENCE ADDRESS:
                             NUMBER OF SEQUENCES:
                                                                                                 APPLICANT:
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                                                                                                Foster, Donald C.
                                                                                                            Cottingham, Ian R. Temperley, Simon M.
                                                                                                                                         Garner,
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 ZymoGenetics, Inc
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; MOLECULE TYPE: protein US-08-756-506-2
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                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sprecher, Cindy A. APPLICANT: Prunkard, Donna E. TITLE OF INVENTION: PROTEIN C TITLE OF INVENTION: ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                   1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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1201 Eastlake Avenue East
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ilarity 70.5%;
Conservative
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                                                                                                                                                                                                                                                                                                             206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.25
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                                                                                           Score 160; DB 2;
Pred. No. 3.1e-19;
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                                                                           Mismatches
                                                                                                           Length 460;
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                                                                           Indels
                                                                         0,
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STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 95-28
FELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
ITELEPHONE: 206-442-6678
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
TYPE: TYPE: protein
US-08-756-506-4

81.28; Score 160; DB 2; L
                                                                                  Query Match 81.2%; Score 160; DB 2; Length 460; Best Local Similarity 70.5%; Pred. No. 3.1e-19; Matches 31; Conservative 2; Mismatches 11; Indels
0;
                                                                                    Gaps
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Search completed: May 15, 2003, 13:28:55 Job time : 16 secs

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64.5
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/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBW_PUB.ppp:*
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                       GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362588 segs, 96450795 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Sequence 1, Appliance 313, Appliance 313, Appliance 42, Appliance 42, Appliance 42, Appliance 5, Appli Appli Appli Appli Appli Sequence S Sequence Sequence Sequence Sequence Sequence Sequence US-10-182-263-3 US-10-182-263-4 US-10-182-263-5 US-10-182-263-5 US-09-978-917A-4 US-09-978-917A-2 US-09-78-917A-2 US-10-107-122-2 US-10-109-498-1 US-09-759-130B-313 US-09-759-130B-312 US-10-189-123-42 US-09-759-130B-310 US-10-189-123-42 US-09-759-130B-310 US-10-189-123-42

RESULT 2
US-10-182-263-3
Sequence 3, Application US/10182263
Sequence 3, Application No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES

US-09-118-748-2 US-09-884-901-3

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Sequence 356 Sequence 85, Sequence 85, Sequence 85, Sequence 18, Sequence 18, Sequence 18, Sequence 12, Sequence 5, Sequence 5, Sequence 12, Sequence 13, Sequence 14, Sequence 15, Sequence 14, Sequence 15, Sequenc	. 0	
	Length 419 Indels	н 44 Н 44
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109-759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-130B 100-1759-1759 100-175	179; No. 5. matche	FEDVDD
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20 64.5 32.7 95 9 US 21 64.5 32.7 208 9 US 23 64.5 32.7 208 9 US 24 64.5 32.7 208 9 US 25 64.5 32.7 208 9 US 26 4.5 32.7 225 9 US 27 48 24.4 348 10 US 28 48 24.4 1363 9 US 30 47 23.9 117 9 US 31 47 23.9 117 0 US 32 47 23.9 117 0 US 33 4 47 23.9 117 0 US 34 47 23.9 117 0 US 35 47 23.9 117 0 US 36 47 23.9 117 0 US 37 47 23.9 117 0 US 38 47 23.9 1186 9 US 39 47 23.9 1186 9 US 30 47 23.9 1186 9 US 31 47 23.9 1186 9 US 32 47 23.9 1186 9 US 34 47 23.9 1186 9 US 35 47 23.9 1186 9 US 36 47 23.9 1186 9 US 37 47 23.9 1186 9 US 38 47 23.9 1186 9 US 39 47 23.9 1186 9 US 39 47 23.9 1186 US 39 48 44.5 22.3 SERYAR E APPLICANT GETING DATE: 2002-07-22 PRIOR FILING DATE: 2002-07-11 PRIOR FILING DATE: 2002-02-11 PRIOR FILING DATE: 2002-02-11 PRIOR FILING DATE: 2000-03-14 INWBER OF SEQ ID NOS: 12 SOFTWARE: PRECHICH VERSION 3.1 SEQ ID NO 6 LENGTH: 419 TYPE: PRT ORGANISM: Homo sapiens	Match Local Sim	1 ANSFLX ANSFLE
20 64.5 21 64.5 22 64.5 23 64.5 23 64.5 24 64.5 25 64.5 26 64.5 26 64.5 27 48 29 48 29 47 31 47 31 47 32 47 34 47 34 47 35 64.5 36 64.5 36 64.5 48 48 31 47 31 47 32 47 34 47 41 47 42 44 44 55 48	Query Match Best Local Matches 3	
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Publication No. USC030027299A1
GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INFORMION: Protein C or activated protein C-like molecules
FILE REPERENCE: 0219us310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
GURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                     1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                    Score 174; DB 9;
Pred. No. 3.8e-21;
0; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTYOR: PROTEIN C DERIVATIVES
FILLE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION UNDERS: 60/181946
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10182263
; Publication No. US200300223541
; GENERAL INFORMATION:
  NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
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70.5%;
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70.5%;
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SOFTWARE: Patentin version 3.1
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                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-10-182-263-1
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Best Local Similarity
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Best Local Similarity
Matches 31; Conserv
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US-09-978-917A-4
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                                           SEQ ID NO 5
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Pred. No. 3.8e-21;
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Pred. No. 3.8e-21;
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                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gerlitz, Bruce E
APPLICANT: Gones, Bryan E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR PLILING DATE: 2000-03-11
PRIOR FILING DATE: 2000-03-14
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTYOUR PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
                                    CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR PLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10182263 Publication No. US20030022354A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10182263 Publication No. US20030022354A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                      Matches 34; Conservative
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US-10-182-263-3
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US-10-182-263-4
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Best Local Similarity
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Best Local Similarity
Matches 34; Conserv
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                                    APPLICANT: MCCATCHY, Jeanette
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MAI-007
CURRENT APPLICATION NUMBER: US/10/017,122
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/327,487
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20030044908A1

GENERAL INFORMATION:
APPLICANT:
PETSSON, EGON
TITLE OF INVENTION: Coagulation Factor VII Derivatives
TITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6286_200_US
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT APPLICATION NUMBER: 60/281,261
PRIOR FILING DATE: 2001-04-03
PRIOR PELICATION NUMBER: PA 2001 00477
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 20
SOFTWARRE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFW 101
                                                                                                                                                                                                                                                                                                                                                    Score 99; DB 9; Le
Pred. No. 1.8e-08;
4; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRIKLFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.7%; Score 96; DB 70.7%; Pred. No. 5e-0 tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION: (1)...(406)
COTHER INFORMATION: Xaa - Any Amino Acid
US-10-109-498-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 313, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCařthy, Sean A
Fraser, Christopher
Sharp, John D
                                                                                                                                                                                                                                                                                                                                                       50.3%;
Publication No. US20030087244A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barnes, Thomas S
Kirst, Susan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mackay, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.7
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 48.8
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-017-122-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-759-130B-313
                                                                                                                                                                                                                    SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-109-498-1
                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219ua310 - protein C
CURRENT APPLICATION NUMBER: U5/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 461
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Pred. No. 9.5e-19;
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1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 160; DB 9;
Pred. No. 9.5e-19;
2; Mismatches 11
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                                                                                                                                                                             APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: 05/181948
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.2%; Score 160; 70.5%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09978917A Publication No. US20030027299A1 GENERAL INFORMATION:
                                                                                                                        Sequence 2, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/10017122
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ilarity 70.5%;
Conservative
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Matches 31; Conservative
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LOCATION: (43)...(461)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SIGNAL LOCATION: (1)...(42)
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                                                                                                    US-10-182-263-2
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PREVENTIVE, THERAPEUTIC, AND OTHER
                                                        Gaps
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       Length 96;
                                                      Indels
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                                                                                                                                      36 NRFDLELFTPGNLERECNEELCNYEEAREIFVDEDKTIAFWQEY 79
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                                                                                                     2 NSF-LXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
Score 84.5; DB 9;
Pred. No. 9e-07;
3; Mismatches 18;
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Pred. No. 2.1e-06;
8; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ... 2002-09-16
... DATE: 2000-09-16
... DATE: 2000-01-07
APPLICATION NUMBER: US 09/479,245
... OR FILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-07-14
PRIOR PELING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1999-07-14
PRIOR PRIOR PAPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROGNOSTIC, DIAGNOSTIC
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Millennium Pharmaceuticals, Inc.
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TITLE OF INVENTION: NOVEL GENES ENCODING PR
TITLE OF INVENTION: PRESNOSTIC, DIAGNOSTIC
TITLE OF INVENTION: USES.
FILE REFERENCE: MPT00-5550MNIM
CURRENT APPLICATION UNBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
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PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                          Sequence 312, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          McCarthy, Sean A
Fraser, Christopher C
Sharp, John D
Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-10-189-123-42
Sequence 42, Application US/10189123
  Query Match 42.9%;
Best Local Similarity 38.6%;
Matches 17; Conservative
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38.6%;
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Wrighton, Nicolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodearl, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.9
Best Local Similarity 38.6
Matches 17; Conservative
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US-09-759-130B-312
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SEQ ID NO 312
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APPLICANT: HOLTZMAN, Douglas A.
APPLICANT: FRASER, Christopher C.
APPLICANT: FRASER, John D.
APPLICANT: BARNES, Thomas S.
TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER FILE REFERENCE: 10147-1103
CURRENT APPLICATION NUMBER: US/10/189,123
CURRENT FILING DATE: 2002-07-02
                                                                                                                            THERAPEUTIC, AND OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                     APPLICANT: HOLLZMAN, DOUGHAS A TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NSF-LXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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Pred. No. 9e-07
8; Mismatches
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PRIOR APPLICATION NUMBER: 08 09/596,194
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
SEQ ID NO 43
LENGTH: 96
                                                                                                                                                                     FILE REFERENCE: MPIO0-5350MNIM
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                      PRIOR PELLING DATE: 100.0-03-10.

PRIOR PELLING DATE: 2000-01-07

PRIOR APPLICATION NUMBER: US 09/479,249

PRIOR PELLING DATE: 2000-04-27

PRIOR PELLING DATE: 2000-04-27

PRIOR FILING DATE: 2000-05-24

PRIOR PELICATION NUMBER: US 09/578,063

PRIOR PELICATION NUMBER: US 09/333,159

PRIOR PELING DATE: 1999-06-14

PRIOR PELING DATE: 1999-06-14

PRIOR PELING DATE: 1999-06-29

PRIOR PELING DATE: 1999-06-30

PRIOR PELING DATE: 1999-09-10

PRIOR PELING DATE: 1999-10-19
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030082586A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.6%;
Matches 17; Conservative
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Gaps

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1;
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Best Local Similarity 38.6%; Pred. No. 2.3e-06;
Matches 17; Conservative 8; Mismatches 18;
                                                     NUMBER OF SEQ ID NOS: 460
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 310
LENGTH: 226
  PRIOR APPLICATION NUMBER: US 09/420,707 PRIOR FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May 15, 2003, 13:29:21
Job time : 20 secs
                                                                                                                                                                                           ; ORGANISM: Homo saptens
US-09-759-130B-310
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                                                                       APPLICANT: HOLTZIAN, Douglas A.
APPLICANT: FRASER, Christopher C.
APPLICANT: FRASER, Christopher C.
APPLICANT: FRASER, Christopher C.
APPLICANT: BARNED, John D.
TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER FILE REFERENCE: 10147-1103
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR APPLICANTON NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES.
THE REPERENCE: WPTOO-25350MIM
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT APPLICATION NUMBER: US/09/759,130B
PRIOR FILING DATE: 2000-01-07
PRIOR PAPLICATION NUMBER: US 09/559,497
PRIOR PALING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR PILING DATE: 2000-05-24
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PRIOR PLILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-04-27
PRIOR PLICATION NUMBER: US 09/559,497
PRIOR PELLING DATE: 2000-05-24
PRIOR PELLING DATE: 2000-05-24
PRIOR PELLING DATE: 2000-05-34
PRIOR FILING DATE: 1999-06-14
PRIOR PLILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR PLILING DATE: 1999-09-10
PRIOR PLILING DATE: 1999-09-10
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Fraser, Christopher C
Sharp, John D
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SOFTWARE: Patentin version 3.1
SEQ ID NO 42
LENGTH: 209
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Myers, Paul S
Leiby, Kevin R
Wrighton, Nicolas
Publication No. US20030082586A1
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                                                           APPLICANT: KIRST, Susan J.
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US-10-189-123-42
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